## 94<sup>th</sup> Annual Meeting of the Pennsylvania Academy of Science

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# **Abstract Book**

### Alternative Energy Symposium ABSTRACTS

#### Listed in order of Presentation

**Black, Brian\*** PSU-Altoona, Altoona, PA 16601. *Leaping the Gap: Tracing Energy Transitions in World History.* — Regardless of their disciplines, a growing number of scholars now refer to our imperfect moment as the Anthropocene Epoch: a moment marked by Earth being perilously near to various cataclysmic tipping points—largely due to the discernible causality of human activities such as burning fossil fuels—and yet recognizably salvageable, with the help of human ingenuity and insight. In terms of intellectual history, the Anthropocene concept in this vein marks a truly culminating point of our understanding of humans' place in nature. My Comments will seize on this ability of the Anthropocene concept to encompass broad, diverse elements of the human condition and also to allow environmental historians an opportunity, at last, to structure a framework to the human past that more accurately contextualizes our species within behavioral details that overcome political and ethnic borders. Just as the Anthropocene portends a common forecast for the future of all humans, it also affords a way of unifying our pasts.

Brownson, Jeffery\* The Pennsylvania State University, State College, PA 16801. The Solar Ecology Framework: Pathways for Discovery and Well-Being from Light. - For over 10,000 years, the story of solar has been the story of society. Generations of communities around the planet have developed localized preferences for diverse solar goods and services; solar vernaculars tied to salt production, food, wine, hot water, comfortable habitation, and now electric power. Our current bellwether for the broad solar field is photovoltaics (PV), growing at an alarming rate internationally. The PV industry doubles in scale every 1-2 years, and PV modules predictably drop in unit cost following "Swanson's rule" (-20% per doubling). Solar electricity deployment is at the core of new electricity markets across the planet. This surge is transforming energy landscapes, both figurative and literal. My research, in connection with colleagues, has brought together decades of common interests in light and light conversion across many disciplines. Light is fundamental to the way that contemporary society and environmental changes actually work. Microwave ovens? They cook with light. Bluetooth connections? Yes, they are light devices. What about our mobile phones, radios, and thermal imaging cameras? Yes, they too are manipulating light. What do we do with the biggest light source in our galaxy, the Sun, and what do we do with the light that comes from the Earth and the Sky as well? Hence, solar ecology describes the integrative systems study of solar energy conversion systems (plants, buildings, photovoltaics), the resulting goods (food, water, energy) and services (shade, trade, cultures of design) derived from the manipulation and conversion of light, and measurements of the flow of light itself as an energy resource unit. The solar ecology framework has been developed at Penn State as a means to consolidate and integrate decades of research methods, results, and heuristic techniques from diverse disciplines, to push to the frontiers of what can be learned in the from the study of solar energy as a systems science. By naming this work "solar ecology", we have pulled together the latent value that was already there, but not yet developed across society. Thus, solar ecologists are essentially "light wranglers". They measure, manage, and convert light to make life better. They can make technologies better by knowing more about light behavior. They can make new societies work smoother by understanding how to manage and control the changes in light. We will explore a few examples: from human vision, to Zen rock gardens, and of course, PV systems-including how they interact with very large landscapes at the utility scale.

**Giebink, Chris\*** The Pennsylvania State University, State College, PA 16801.*Concentrating sunlight without tracking the Sun.* —Sunlight is a diffuse energy resource and thus all methods of solar energy conversion and use by society share one feature in common – concentration. Optical concentration offers a route to lower the cost of high efficiency photovoltaics, desalinate seawater, and increase biofuel production; however, traditional concentrators rely on expensive mechanical tracking systems and on geometric optics that cannot harvest the diffuse solar component. This talk will focus on recent developments in luminescent and microtracking concentration that address these respective challenges, enabling solar concentration even on cloudy days and opening up a practical pathway to bring the ultrahigh efficiency solar cells used on satellites to your rooftop.

**Asbury, John B.\*** The Pennsylvania State University, State College, PA 16801. *Multi-Exciton Generation Mechanisms: Multiplying the Benefits of Solar Power.* —Silicon solar cells have been developed over the past fifty years and are now a mature technology that has already achieved nearly 90% of their maximum possible solar to electrical power conversion efficiency. The theoretical maximum power conversion efficiency of such solar cells, which is around 30%, is set by the overlap of the broad solar spectrum with the single bandgap of silicon. While solar concentrators and complex device structures involving multiple types of materials can significantly increase the power conversion efficiency of solar power systems, the cost of such systems are often prohibitive for wide-spread use in terrestrial applications. Fortunately, novel photophysical processes can be used to convert high energy excited states formed by absorption of light from the blue region of the solar spectrum into multiple excited states that can then multiply the photocurrent from solar cells. Development of these approaches offers the potential to enhance the efficiency of silicon solar cells while avoiding expensive approaches based on solar concentration or multiple material types. This talk will focus on two such methods of multiple exciton generation using nanoscale materials and conjugated molecules.

**Flarend, Richard\*** PSU-Altoona, Altoona, PA 16601. *Solar Energy and Market Suppression: How solar benefits everyone*. —Solar energy is typically envisioned as a way to help reduce harmful emissions from power plants or, for those more practical minded, as a way to reduce or eliminate your own personal electric bills. Solar energy certainly does accomplish these two goals, but it also has another impact on the electric industry that is not typically examined. Electric distribution companies (EDCs or utilities to the layperson) and electric generation suppliers (EGS or the 'choose your own supplier' company) also benefit a great deal from solar energy.

Research will be presented that shows that these EDCs and EGSs actually benefit more when a customer 'goes solar' and no longer pays a monthly bill than when the customer was a regular bill-paying consumer. Other ratepayers also benefit when a customer decides to 'go solar'. A single family adopting solar energy on their home can reduce the bills of everyone else in the county. The process that accounts for this is called market suppression. A little solar energy at the right times, will actually move the entire electric market by measureable amounts. If just 1% of customers in Pennsylvania use solar energy, the EDCs and EGSs will save 2% on their overall purchases of energy for all their customers. This amounts to about 20x the lost revenue from those solar customers.

Solar incentives do not always reward the few customers who make the expensive switch to solar energy. Nor do current solar incentives properly promote the further growth and infrastructure development that is necessary for large-scale solar adoption (10% or more). This presentation will address how market suppression can be leveraged to encourage a greater level of solar adoption, utility scale storage, and ratepayer savings.

**Welch, Lindsey**\* Cedar Crest College, Allentown, PA 18104. *Sustainable energy through biomass conversion using liquid phase catalysis.* —The growing need for the advancement of renewable energy research is in part due to the overuse of nonrenewable fossil fuels and their impact on the environment. In this presentation, catalytic pathways for the transformation of biomass material to

liquid transportation fuels will be described. The use of homogeneous and heterogeneous catalysts to convert carbohydrates and lipids to fuels is an important area of research that may lead to a better understanding of the fundamental science behind efficient and sustainable energy production. Specific work in the area of oleaginous yeast conversion to biodiesel, solid acid catalysis of pyrolyzed wood, and hydrogenation of carbohydrate-derived biomass will be discussed. This research is ongoing and implements collaborations from other academic institutions within Pennsylvania. Implications of the results of this work will be presented in the context of other leading research in this field.

**Johnstonbaugh, Edward V.\*** Penn State Extension-Westmoreland, Greensburg, PA 15601, *Biochar, the Key to Expanded Biomass Energy Markets.* —The incorporation of renewable energy into the modern practices is driven by the cost advantage the renewable source has over the fossil resource to be displaced. Recent advances in drill technology and production practices have led to a low cost supply of natural gas that has slowed the growth of biomass as a fuel of choice. To reverse the current trend carbon neutral biomass resources need to be restructured to minimize their disadvantages and thereby increase their value on a \$/BTU basis. Torrefaction and/or Pyrolysis of common biomass resources has the potential to increase the value of these fuels by broadening their range of application, and by opening up new markets to replace materials now commonly supplied by fossil resources. In this discussion opportunities to transform carbon neutral biomass fuels into higher value forms that compete directly with fossil fuels will be looked at and debated.

**Wagner, Rachel\*** Saint Francis University Loretto, PA 15940. *Microbial Electrochemical Technologies: Possibilities and Practical Matters.* —Microbial fuel cells convert waste organic matter into electricity using bacteria as the catalyst for the anodic conversion, and oxygen reduction as the cathodic reaction. This technology has potential application for many wastewater-producing industries, including municipal wastewater treatment as well as agricultural, food production, and other industrial wastewater treatment systems. In addition to the electrical current that is produced by these battery-like systems, energy savings are found because of the reduction of energy-demanding processes such as aeration that is common in many wastewater treatment technologies.

In addition to the generation of electrical current that could contribute to the electrical grid or the electrical needs of the wastewater treatment plant, technologies related to MFCs, collectively called microbial electrochemical technologies (METs), are being investigated for the production of manufacturing chemicals such as caustic soda, hydrogen peroxide, and hydrogen gas. Using waste materials as the substrate for the anodic reaction may allow for considerable cost reductions in the production of these chemicals.

**Rohrs, Allison**\* Saint Francis University Loretto, PA 15940. *Status of Wind in Pennsylvania: Overview & Policy.* —Newly constructed wind farms have seen a sharp decline in last five years in Pennsylvania- with only one new utility scale wind farm built since 2013. Windy, undeveloped locations still exist in the Commonwealth, but come with significant hurdles for wind developers. Today's obstacles include access to transmission lines, finding agreeable landowners (both public and private), potential environmental impacts, lack of available long term contracts/power purchase agreements, and community opposition. This presentation will delve deeper into these issues to examine the status and future of wind industry in Pennsylvania.

**Barton, Michael\*** Forestry Consultant Sidman, PA 15955. *Status of Wind in Pennsylvania Part II: Environmental Impacts.* —With the push for renewable energy at the turn of the century wind mills have become a commonplace part of the landscape. Due to their size the turbines have seemingly both social as well as environmental impacts. In order to reduce or negate many of the potentially adverse impacts of wind farm development and operations a number of significant studies are conducted in both the pre and post construction phases of the development process. In this discussion these studies will be reviewed and presented. Many of the preconstruction studies are a requirement in order for wind farm construction to be permitted. Impacts to both wildlife and the landscape can be significantly reduced or eliminated with careful project design; from proper wind farm siting and habitat avoidance measures, through proper erosion control design. This extends through project construction phase; with proper development techniques and implementation practices through the projects active life; with methods of significantly reducing bird and bat impacts through curtailment.

**Sell, Michael\*** Saint Francis University Loretto, PA 15940. *Reaching Sustainability Goals Through Efficiency and Off-Grid Living*. —Off-grid, simplistic living is the foundation of the booming, new "Tiny House" movement. Utilizing technologies such as solar, wind, and biomass, these tiny spaces are generating their own energy to provide modern luxuries in small, simplistic living spaces. According to the U.S. Census Bureau, the average size of a new single-family home encompassed 2,640 square feet in 2016. In contrast, tiny house footprints span no more than a few hundred square feet. While not everyone is rushing off to downsize, tiny house living can offer lessons for more sustainable living. Trends adopted in off-grid design also mirror developments in the larger grid system, which is increasingly turning to renewable technologies, higher efficiency and the deployment of energy storage. This movement inspired the SFU Institute for Energy to design and construct a tiny, mobile classroom/lab to use both as a demonstration of different renewable energy technologies as well as an environment for teaching about such technologies.

## **General Meeting ABSTRACTS**

#### Listed alphabetically by first author's last name.

**Abreu, Leslie\*, Jean-Francois Therrien, and Allison Cornell** Cedar Crest College, Allentown, PA 18104. *Interannual variation in diet composition of American kestrel (<u>Falco sparverius</u>) chicks. — American kestrels are cavity-nesting birds which readily utilize man-made nest boxes. Their generalist diet ranges from invertebrates to small rodents and birds. The degree of variation in diet between chicks of different nests and across years is not well understood. The purpose of this study was to analyze how diet varies across individual breeding pairs of American kestrels, and how diet composition changes across years. We thus studied pellets of undigested material from breeding diet of kestrels in a network of nest boxes located around Hawk Mountain Sanctuary, PA, from 2012 to 2017. Preliminary results on 27 dissected nests indicate that prey composition varied widely between individual nests. Individual nests were composed of 0-96% insect prey compared to vertebrate prey items (4-100%). Across years, average use of insect prey items ranged from 24-66% use. This project will further explore how annual and individual variation contribute to diet. (28)* 

Adams, Haley\*, and Cynthia Walter Saint Vincent College, Latrobe, PA 15650. The Relationship of Water Quality and Season for Privately-Owned Water in Southwestern Pennsylvania. - Privatelyowned water (POW) is not regulated by the federal or state government, whereas municipality water (MOW) is regulated on state and federal levels. Pennsylvania has over 3 million people who rely on POWs. My goal was to monitor water quality in twenty POWs in two seasons. The water was tested for fecal coliform bacteria, hydrogen sulfide producing bacteria (HSPB), total chlorine, iron, fluoride, bromide, chloride, nitrate, nitrite, phosphate, and sulfate concentrations at two different sources for POW per home. The water was sampled during the high rainfall in May and low rainfall in September 2017. In 7 of 11 POW households, conductivity increased by 200 uS/cm during the dry compared to wet season. No households exceeded the limit of conductivity or total dissolved solids. Of the 15 POW households that were tested in the wet season, 7 households (47%) had positive Escherichia coli within 24 hours of sampling and 3 additional households (67%) had positive E. coli within an additional 24 hours of sampling. Of the 16 POW households that were tested in the dry season, 7 of 11 households (44%) had positive E. coli within 24 hours of sampling. For HSPB 27% of households had a positive assay in the wet season and 44% of households with positive HSPB during the dry season. Study households had not been tested for at least 10 years. No households had any antibacterial treatment mechanisms. Having any kind of contaminated water, or water that does not meet the recommendations at either the state or federal level, could cause many illnesses including gastrointestinal illnesses. My observations are consistent with a larger study done across Pennsylvania. Homeowner education on the need to test water and actions to treat well water would improve drinking water quality. (153)

**Aljagthmi, Wafaa\*, and Cuong Diep** Indiana University of Pennsylvania, Indiana, PA 15705. *Determining the effect of the R1 peptide on lhx1a dimerization*. — Kidney disease is a major health problem and current treatments for kidney failure are expensive and have severe limitations. Therefore, an alternative therapy such as stem cells/regeneration is needed. Zebrafish kidney stem cells express the *lhx1a* gene, which is essential for kidney development and regeneration. We found that *lhx1a* dimerizes with itself in a genetic assay and hypothesize that dimerization is important for its activation as a transcription factor. A genetic screen was carried out and the R1 peptide was found to bind to *lhx1a*. The goal of this project is to determine whether the R1 peptide affects *lhx1a* dimerization. If so, the peptide could serve as a new tool for modulating the function of *lhx1a*, which would provide insights into the molecular function of *lhx1a* during kidney development and regeneration. (**70**)

**Allen, Aleique\*, and Clint Jones** Mercyhurst University, Erie, PA 16546. *Electrochemical analysis of natural antioxidants in different types of tea.* — Tea is consumed by many people in the world. There are different types such as black, green, oolong and white tea, and all of them contain polyphenols that contribute to the antioxidant activity of teas. The polyphenols are sub-divided into flavan-3-ols and flavonols. The different types of tea will be studied for its antioxidant activity by using cyclic voltammetry. An Ag/AgCl KCl saturated electrode acts as reference, Pt wire as the counter and a glassy carbon electrode as the working electrode. Three different samples of each type of tea will be brewed according to instructions and then diluted 100-fold in a pH 7 phosphate buffer solutions. Currently green tea demonstrates the greatest antioxidant ability with the lowest average peak anodic voltage of 275.31 mV. Continuing analysis of the teas will help to determine the teas with the greatest antioxidant potential. (**168**)

**Almony, Sarah\*, and Stephanie Justice-Bitner** Kings College, Wilkes-Barre, PA 18711. *Detection of novel cannabinoid receptor 1 (CB1R) interacting proteins.* — The physiological effects of  $\Delta$ 9 – tetrahydrocannabinol (THC), the cannabinoid ligand known to be the main active component in marijuana, are mediated through its binding to receptors in the endocannabinoid system. A biochemical cascade occurs via the cannabinoid-1 receptor (CB1R) located in regions of the brain associated with memory, motor function, reward processes, and motivation. The binding of THC and other cannabinoid ligands to the CB1R occurs at the carboxyl terminus of the receptor. This signaling process requires the use of many known and unknown proteins. We have utilized a yeast-2-hybrind (Y2H) screen using short intracellular amino acid sequences of the C-terminus of the CB1R in order to determine the presence of novel CB1R-protein interactions. Any confirmed interactions could lead to future studies on the development of pharmacotherapies as an approach to modulate and treat addiction, as well as other disorders that arise from abnormalities in the brain's ability to regulate reward and motivation processes. (97)

AlMuhanna, Mohammed\*, and Robert Hinrichsen Indiana University of Pennsylvania, Indiana, PA 15705. The disruption of the phototransduction process in the planarian Schmidtea mediterranea and its effect on phototaxis. - Phototransduction is a cell signaling process utilized by a broad array of organisms to response to light. In higher organisms, a cGMP-gated ion channel is utilized by retinal cells to transduce the photon-induced signal to the brain. The invertebrate planaria Schmidtea mediterranea displays a negative photoresponse, which allows it to locate optimal environments. This project was designed to determine if the cGMP-gated ion channel is required for the planarian photoresponse. Therefore, a cGMP-gated ion channel homologue was identified and cloned from Schmidtea mediterranea; this gene was then used to inhibit its expression by means of RNA interference. In order to perform RNA interference, whole RNA and mRNA were isolated and the mRNA was used to synthesize cDNA. The cDNA was then employed to amplify the gene for cGMP-gated ion channel from planarian. The amplified DNA was cloned into a pGEM-T vector and the DNA from the insert was sequenced to insure the proper gene had been cloned. New primers were synthesized, which included T7 promoter sequences, and these were used to amplify the gene. The purified PCR product was then used to synthesize dsRNA using T7 RNA polymerase. The dsRNA was added to liver paste (the food source of planaria) and the worms were fed over a two week period. The worms will be tested for two different biological processes: 1) the viability and growth of the worms; and 2) the ability to the planaria to respond to bright light. A photoresponse assay has been developed, which will allow for the quantitative analysis of the response to light when the cGMP-gated ion channel is not expressed. (90)

Alnajjar, Roaa\*, Seema Bharathan, and Narayanaswamy Bharathan Indiana University of Pennsylvania, Indiana, PA 15705. *Characterization of Double-stranded (ds) RNA from the plant pathogenic fungus <u>Rhizoctonia solani</u>. — Rhizoctonia solani,* which causes a number of diseases in crops, is a soil-borne plant pathogenic fungus. *R. solani* is a complex species recognized by its Anastomosis groups (AG's), which has fourteen different groups in total. The ability of some fungi to cause disease is greatly reduced due to viral infection. The genetic material double-stranded (ds) RNA from these viruses have been implicated in reduced pathogenic ability. This research focuses on isolate EGR-4, which is homokaryon, belonging to the Anastomosis groups (AG2). The main objective of this project is to develop primers for the cloned sequence and perform Real-Time PCR to test viral dsRNA. In order to find this objective, double-stranded (ds) RNA of 3.8 to 4 kb of EGR-4 was extracted by using phenol and CF-11 cellulose powder. The dsRNA was reverse transcribed into cDNA and ligated into a p-jet clone vector. The plasmid was further purified for three different clones- EGR-4.3, EGR-4.4 and EGR-4.5 by using a fast digest enzyme EcoRI. The gel electrophoresis showed that EGR-4.5 is the larger fragment containing full length cDNA. The cloned fragment was sequenced by a Sanger sequencing sequencer (Retrogen, Inc. USA). Following sequencing the forward primer, reverse primer, and the probe were designed to test viral dsRNA. The forward primer (CGGCGGTCTGATGATAGC) and reverse primer

(CGCAAGGATAATCGGGCATTC) were used to amplify dsRNA from purified EGR-4. The PCR products ranged between 2.2 and 2.6 kb. The sensitivity of detection of EGR-4 dsRNA was further enhanced by di-hybrid probes. The probe sequence included (5'Fam-

TGACACATTCGCAGATCGAGTACATGG-BHQ1). The results from q-PCR, and sensitivity of detection including those from conventional PCR will be presented. (84)

Arnold, Victor\*, and Julie Belanger Kings College, Wilkes-Barre, PA 18711. Optimization of lipid production through sonication and extrusion. - Phosphatidylcholine (PC) is a class of phospholipid that contains choline as a head group and is a major component of most biological membranes. Due to its abundance, PC lipid can be extracted from naturally occurring resources such as meat, nuts, and eggs. Within the context of this experiment PC lipid was extracted from eggs, and then used to create liposomes using phosphate buffered saline (PBS). The production of liposomes was mainly performed through two methods, sonication and extrusion. Both methods were compared for their ability to turn multilamellar liposomal suspensions into unilamellar liposomal suspensions. Ideally, the most efficient method should give reproducible results with small liposome size and particle distribution. Initial tests suggest two conclusions, both methods are comparable in effectiveness, however sonication produces more uniform suspensions, while extrusion reduces radius size more significantly. For example, extrusion of a liposomal suspension produced liposomes with a radius of 45.8 nm with 29.6% polydispersity; while sonication produced liposomes with a radius 99.1 nm with 45.6 % polydispersity. The addition of cholesterol and its effects on liposomal suspensions, as well as creating alternate methods to produce small unilamellar vesicles continue to be explored. (160)

Ash, Michelle\*, and Jeffrey Stephens Misericordia University, Dallas, PA 18612. Exploring the dimorphic nature of C. albicans through atomic force microscopy. - The common yeast Candida albicans resides within the human body in its wild-type form. As a developing pathogen in basic pH, the typically ovoid cells of C. albicans begin to form germ tubes that eventually grow into hyphae, allowing the cell to burrow into soft tissue. In addition, another morphology forms at acidic pH, known as the pseudohyphal variety, in which the cells never cleave off after budding, giving rise to a tail-like chain of cells. Due to the growing prominence of blood-borne yeast infections in the United States, research to combat C. albicans' pathogenicity has increased dramatically. Atomic force microscopy has the unique ability to perform force-distance spectroscopy on materials, calculating their relative stiffness; biophysicists utilize this tool to determine cell stiffness and perform analysis related to cellular mechanics. The atomic force microscope also serves as powerful imaging tool to provide precise images of molecules and cells on a small scale. Our research findings determined the absence of a fundamental difference in the stiffness between the pseudohyphal and wild-type morphologies of Candida albicans; this data gives insight into how the cell membrane changes in reaction to the growing germ tubes. These findings are within our expectations, since no appendage of the cell is formed in the pseudohyphal morphology, simply the appearance of one from a long chain of cells that have not undergone cytokinesis. Images of the treated cells have confirmed morphological presence, and resolved physical characteristics that

define each morphology. Our analysis of the hyphal morphology is ongoing and will continue throughout the course of 2018. (94)

Atondo, Jamie\*, and Jeff Newman Lycoming College, Williamsport, PA 17701. Chryseobacterium JAH sp. nov., isolated from a freshwater creek. – Chryseobacterium sp. JAH was isolated from a freshwater creek in Montoursville Pennsylvania as part of an undergraduate microbiology course at Lycoming College in January of 2015. Chryseobacterium sp. JAH was gram-negative, non-motile, non-spore-forming rods, that produced yellow-pigmented colonies on nutrient agar. The most abundant fatty acids were iso-C<sub>150</sub> and iso-C<sub>170</sub>3OH. Phylogenetic analysis based on 16S rRNA gene sequencing showed that the strain was most closely related to Chryseobacterium sp. YR005, Chryseobacterium greenlandense UMB34, and Chryseobacterium aguaticum KCTC (99.24, 97.84, and 97.57 sequence similarity). The combined genotypic and phenotypic data supported the conclusion that the strains represent a novel species within the genus Chryseobacterium. While characterizing Chryseobacterium sp. JAH, it was noted that there was little difference between the 16S rRNA sequences of Chryseobacterium aquaticum KCTC and Chryseobacterium greenlandense UMB34. The 16S rRNA gene sequences were 99.24% similar, AAI was 98.8% similar, ANI was 98.9% similar and GGDC was 90% similar. These values are higher than the species threshold for these metrics, suggesting that these two should be classified as the same species, just different strains. We propose that Chryseobacterium greenlandense UMB34 be reclassified as a strain of Chryseobacterium aquaticum. (16)

Ayer, Danielle\*, and Ryan Colyer Cabrini University, Radnor, PA 19087. Construction and characterization of an open body fluorescence microscopy system for fluorescence lifetime imaging. - This project presents a custom system that is used for detection and acquisition that is integrated with optical components, a prototype photon detector, and custom electronics. This microscope uses a laser to excite fluorophores in order to count the individual photons by using compressive sensing and lifetime imaging. To produce an image, compressive sensing uses multiple mirrors and a point detector. Lifetime imaging determines each pixel color in an image from the amount of time that it takes for electrons, which were excited by a laser, to return to the ground state of the fluorophores. Our method under development propagates fluorescence lifetime through compressive sensing in order to use a single point detector to efficiently produce a full lifetime image. A primary goal of this project is to construct a sturdy light-tight enclosure for an open-body custom microscope. This enclosure will allow the insertion of samples while also blocking out ambient light during acquisition. Another, main goal of this project is to characterize the performance of the system under development using measurements of fluorophores. This will be done by performing a variety of measurements that will characterize the response to different light intensity levels. These measurements will also examine the time response of fluorophores with various fluorescence lifetimes. The measurements will be used to construct phasor plots of fluoresce lifetimes which will be used for the later compressive sensing system. This project is looking to produce a novel and cost-efficient design for acquiring fluorescence lifetime images with low light conditions, which are favorable for examining biological samples. (89)

**Barbarich, Tara\*, Hailey Shannon, Cutter McMinn, and Matthew Persons** Susquehanna University, Selinsgrove, PA 17870. *Burrowing and escape responses among riparian and nonriparian populations of wolf spiders.* — Many riparian species have evolved adaptations to respond to rising water either through avoidance or submersion tolerance. We examined differences in submersion tolerance and burrowing behaviors among riparian and non-riparian populations of different wolf spider species. Five wolf spider species from riparian or non-riparian populations were submerged for three hours under water and recovery latency was measured (N=492). We also measured maximum burrow depth and escape behaviors of three species of burrowing wolf spider from riparian and non-riparian populations during a simulated flood event (N=90). Riparian wolf spiders had significantly shorter recovery times from submergence than non-riparian populations of the same species. We also found no significant differences across species in submergence tolerance. Of the three burrowing species, riparian spiders showed a marginally non-significant trend toward shorter escape times from burrows during simulated flooding and tended to have shallower burrows than the same species from non-riparian populations, however we found significant species differences in flood response that masked differences in riparian and non-riparian populations. Overall, riparian wolf spider populations appear to have evolved higher submergence tolerance and quicker escape responses during flood events compared to non-riparian populations. Most spiders did not use their burrow as a physical gill, but some individuals did stay submerged within their burrows for more than six hours before leaving. This suggests that waiting until the water level retreats may be an alternative strategy to cope with flooding. Overall, our study indicates that wolf spider communities likely persist during flood events rather than being extirpated and recolonized by new spiders from other areas. (40)

**Barnhart, Ryan\*, Deanne Cuda\*, and Sudipta Majumdar** Indiana University of Pennsylvania, Indiana, PA 15705. *Killing <u>Klebsiella pneumoniae</u>, a fight against antibacterial drug resistance.* — *Klebsiella pneumoniae* is a gram-negative bacterium responsible for multiple healthcare infections such as pneumonia, bloodstream infections, and surgical site infections. Every year approximately 450 million people die from pneumonia. Some forms of *Klebsiella pneumoniae* strains are highly resistant to antibiotics. They are able to produce an enzyme known as carbapenemase which make it resistant to the carbapenem antibiotics, which is often used as the last line of defense against this bacteria. Therefore, it is important to research new ways to combat this infectious disease. This may be done through the inhibition of the alanine racemase enzyme that is used by the bacteria to convert L-alanine to D-alanine, which is an essential building block for bacterial cell wall biosynthesis. *Klebsiella pneumoniae* codes for two alanine racemase genes. Our research is focusing on cloning both genes in order to express, purify and characterize the associated enzymes. **(15)** 

Barr, Stephanie\*, and Andre Walther Cedar Crest College, Allentown, PA 18104. Development of a High Resolution Melt (HRM) analysis tool to genetically fingerprint beer yeasts. — Beer is one of the most popular alcoholic beverages in the United States. In 2011, Americans drank an estimated 6.3 billion gallons. The brewing process involves making a malt, which is a solution of sugars extracted from a grain that can then be fermented by yeast that convert sugars into carbon dioxide and ethanol. Two of the most common yeasts used are Saccharomyces cerevisiae, used to brew ale beers, and Saccharomyces pastorianus, used to brew lager beers. The different strains lead to a different flavor, color, and alcohol produced so it is essential that the proper yeasts are used to brew each type of beer. In large breweries, sometimes the wrong yeast can contaminate the batch of beer. Large breweries reuse the yeast multiple times (re-pitch) so eventually an insignificant amount of contamination can completely ruin an entire batch. Current tests for contamination can take up to a week to obtain results, which wastes time, money, and resources. My research focuses on creating a new protocol that large beer companies can use to test for contamination in their batches of beer using a quantitative polymerase chain reaction (qPCR) with high resolution melt point analysis (HRM). The PCR primers target short tandem repeat sequences on the S. cerevisiae or the S. pastorianus genome. As the DNA is amplified, the HRM is used to identify the melting points of the different strains. This process can be used to identify small amounts of contaminations before they cause major contamination in the beer. (23)

**Belanger, Julie\*, Joseph Cirilo, and Thomas Reidy** Kings College, Wilkes-Barre, PA 18711. *Characterization of unexpected meta-stable dispersions inspired by the Greek drink, Ouzo.* — Previous research has used poorly water-soluble or hydrophobic compounds to explore novel ways to make inactivated vaccines using enveloped viruses. Hydrophobic compounds are also routinely used in aqueous environments in cell-based assays for cell differentiation or drug delivery assessment. These hydrophobic compounds are typically first dissolved in a water-miscible organic solvent before they are introduced into the aqueous environment. This is true for studies involving cell lines or enveloped viruses, where the goal is to introduce the hydrophobic compound into the membrane bilayer. Our research has found that when naphthalene-derived hydrophobic compounds are first dissolved in a water-miscible solvent, and subsequently added to water, a metastable dispersion forms. This dispersion does not form if the compound is simply added to water, or to a mixture of water + miscible organic solvent. The underlying mechanism for the formation of these dispersions is presumably through the "Ouzo effect", named after a Greek drink of the same name. The particles that are suspended in these dispersions, result from the initial formation of solution droplets (containing solvent and hydrophobic compounds) that fairly rapidly create supersaturated droplets of solution via solvent-shifting. The metastable nature of this colloidal dispersion allows it to be stable for days with particle sizes on the order of 400 nm (radius). The concentrations used in this study were comparable to those used in previous cell-based and virus-based studies. Characterization of the formation, stability, and particle sizes of these dispersions will be discussed. (1)

**Berkheimer, Colin\*, Tessa Woods\*, Krista Silvis, Rachel Mills, and Edward Levri** Penn State University-Altoona, Altoona, PA 16601. *Habitat type and the interaction between the invasive New Zealand mud snail and native gastropods in Polecat Creek, Wyoming.* — The New Zealand mud snail (*Potamopyrgus antipodarum*) is a world-wide invasive species and is very abundant in the Greater Yellowstone Ecosystem. In Polecat Creek, Wyoming, densities of the invader have been recorded up to 700,000/m<sup>2</sup>. In its native New Zealand, the snail varies in density and life-history characteristics by habitat within the same water body. The purpose of this study is to determine if there are differences between New Zealand mud snails inhabiting different habitats within Polecat Creek. Here we compare the ratios of *P. antipodarum* to native gastropods within three different habitats (stream bank, reeds, and macrophytes). A preliminary analysis of the data suggests that there are significant differences in the proportion of New Zealand mud snails in the three habitats compared to native gastropods, and that these differences may result in different life history measures between habitats. (**142**)

Blaetz, Margaret\*, Jeannie Showers, Christopher Pagan, and Ellen Yerger Indiana University of Pennsylvania, Indiana, PA 15705. Variation in insect herbivory in common garden plots in *different ecosystems.* — Many ecosystems are invaded by non-native plants, which grow so abundantly that they overtake native plants and replace them. The mechanism for this dominance by non-native plants is still unresolved, although several theories have been advanced, one being the Enemy Release Hypothesis. The Enemy Release Hypothesis predicts that invasive plants are released from insect herbivory in the new ecosystem and experience less biomass loss than native plants. This is because the insect herbivores are not transported to the new ecosystem, so the plant is "released" from herbivory. To test this reason for invasive plant success, missing leaf area was compared for pairs of closely related native versus non-native plants in a common garden. This study compared locally abundant invasive honeysuckle leaves. Lonicera morrowii, to its native congener L. sempervirens, and also compared invasive multiflora rose leaves, Rosa multiflora, to its native congener R. carolina. Our results show that insect herbivory levels vary widely for different plot locations, even when each plot was planted in an identical common garden design. For honeysuckle, insects removed less leaf area from invasive plants growing in our Natural Area plot, more in our Farm plot, and the same as native plants in our Suburban plot. This variation does not support the Enemy Release Hypothesis, and suggests that herbivory depends most on the surrounding ecosystem. (62)

**Bond, Derrick\*, Drew Hannon\*, and Sudipta Majumdar** Indiana University of Pennsylvania, Indiana, PA 15705. *Cloning of Alanine Racemase from two different pathogenic bacteria <u>Enterococcus faecium</u> and <u>Neisseria gonorrhoeae</u>. — Antibacterial resistance has become one of the most prevalent issues facing global public health. It poses problems in effectively preventing and treating an increasingly wide range of bacterial infections. Because of this, there is a pressing need for new antibacterial targets and drugs. One of these identified targets is alanine racemase (Alr), an enzyme which is required by all bacteria for cell-wall biosynthesis. Alanine*  racemase is a very attractive drug target because of the fact that it is essential for bacteria while it is not present in humans. Therefore, inhibiting alanine racemase will eliminate bacteria while leaving the human host unharmed. In this project, alanine racemase from pathogenic bacteria grampositive *Enterococcus faecium* and gram-negative *Neisseria gonorrhoeae*, responsible for causing bacterial endocarditis and sexually transmitted gonorrhea, are cloned in order to allow for further study and characterization of the enzyme. (91)

Brady, Caleb\*, Shannon Johns, Aaron Wolfe, Michael Tyree, Jeffrey Larkin, Scott Eggerud, and Michael French Indiana University of Pennsylvania, Indiana, PA 15705. Survival and Growth of <u>Castanea</u> dentata Planted at the Flight 93 National Memorial. — The Flight 93 National Memorial, located in Somerset County, PA was established on a reclaimed surface mine which was recontoured and seeded in the mid 1990's. For the last six years (2012-2017), the National Park Service, Office of Surface Mining Reclamation and Enforcement, and hundreds of volunteers have been planting native trees and shrubs in a large reforestation effort. To date, six phases have been planted with a total of 102,393 trees and shrubs including 5,938 potentially blight-resistant American chestnut backcrosses (Castanea dentata (Marsh.) Borkh) provided by The American Chestnut Foundation. Two-hundred sixteen permanent plots were established to monitor plant growth, health, deer browse, and competition across the planting phases. Average survival of A. chestnuts across all six phases was 47 and 42% in the summer of 2017 and 2015, respectively. Growth rates across Phases I-IV were 0, 4, 4, and 1 cm yr<sup>-1</sup>, respectively. American chestnuts showed extremely low levels of deer browse with 96% showing no or only slight (< 1/3 stems) browse. Individual tree health was measured gualitatively on a scale of 0-4, with zero meaning the plant is dead and 4 meaning it is healthy and vigorous. Across the entire site approximately 85% of surviving A. chestnuts were rated as healthy (Vigor score of 3 or 4). These data show that the American chestnut backcrosses Castanea dentata (Marsh.) Borkh are capable of growing healthfully in certain surface mined soils. If future data shows that The American Chestnut Foundation's backcross chestnuts are indeed blight-resistant and can begin reproducing naturally, this could mean that the goals of reestablishing wild American chestnut trees and reforesting land that has been surface mined could be combined into one restoration effort. (45)

Budzilowicz, Amanda\*, Bianca Santos, and Joyce Belcher Cabrini University, Radnor, PA 19087. Regulatory effects of ellagic acid on bone-forming osteoblast and bone-resorbing osteoclast cells. - Bone is a dynamic organ that is responsible for vital mechanical and metabolic functions, and is continuously being remodeled by osteoblast and osteoclast activity to maintain normal bone mass. While osteoblasts are the bone forming cells, osteoclasts are the bone resorbing cells. Normal bone homeostasis has balanced osteoblast/osteoclast activity. Bone remodeling imbalances can be caused by excessive resorption or excessive bone formation activity, leading to bone disorders such as osteoporosis, osteopetrosis, and Paget's disease. Studying the biological regulatory mechanisms and irregularities in the proliferation and differentiation of osteoblasts and osteoclasts in vitro could help better diagnose and treat bone loss disorders. Treatment for osteopenic diseases often uses pharmaceutical agents, such as bisphosphates, that can be poorly tolerated and have adverse side effects. Recent research has led to the use of phytochemicals as a possible agent to treat bone disorders, due to their anti-inflammatory and antioxidant properties. The present research examined ellagic acid (EA) on 7F2 osteoblasts and osteoclast induced RAW264.7 cells lines. Both osteoblasts and osteoclasts were treated with low (10µM) and high (20µM) doses of EA. The cell types were treated with EA, and various assays were performed to examine the effects the treatment had on key markers of proliferation, differentiation, and cellspecific function. Low and high doses of EA proved to be non-toxic on both 7F2 and RAW264.7 cells. The EA treatment of 7F2 cells proved to be successful in increasing proliferation, calcium deposition, mineral deposition, and ALP activity versus control groups. EA treatment on osteoclast induced RAW264.7 cells had no differences in TRAP activity and TRAP+ cell count versus the control. EA was able to stimulate positive markers of osteoblast cells while not affecting osteoclast

proliferation or enzyme degradation activity. Treatment with EA could provide a significant therapeutic impact versus traditional pharmaceutical agents for bone disorders. (50)

Buell, Chelsea\*, Morgan Eytcheson, Joseph Duchamp, Gregory Turner, Jeffrey Larkin, and Michael Tyree Indiana University of Pennsylvania, Indiana, PA 15705. Allegheny woodrat (Neotoma magister) food preference: A comparison of American chestnut hybrids and native oak nuts. - The loss of the American chestnut [Castanea dentata (Marsh.) Borkh.] as a hard mast producer has had a major impact on the ecology of the Appalachian forests. It has been suggested that chestnut fruit may have been an important food source for the Allegheny woodrat (Neotoma magister), a species that has been experiencing consistent long-term populations declines throughout much of its historic range. Re-establishing blight-resistant, hybrid chestnuts may return an important food source however, few studies have examined Allegheny woodrat food preferences. We conducted field experiments to examine if Allegheny woodrats exhibit a preference to hybrid American chestnut fruit over white (Q. alba L.) and northern red oak (Q. rubra L.) acorns. Secondly, we examined if short-term, repeated encounters could change food selection behavior. We implemented a reduced cafeteria-style test over consecutive nights at four locations in central and western Pennsylvania. Preliminary results show that the hybrid chestnut is preferred over white oak. Findings from our study will provide insight regarding the future benefits of American chestnut restoration on woodrat conservation. Allegheny woodrats preference of hybrid American chestnuts suggests a strong potential for chestnut restoration at habitat sites to address periodic food limitations that are known to influence the species' demographics. (46)

Burns, Jessica\*, Emily Rollinson, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301. Habitat preferences and species distribution models for bats in the Delaware Water Gap National Recreation Area. - Following the arrival of the fungal disease Whitenose Syndrome (WNS) in North America in 2006, massive mortality of hibernating bats has made the conservation of these species a critical concern. Improvements in technology for acoustic monitoring and automated call classification have led to new survey methods to assess bat population status and distribution. One new survey technique, mobile acoustic transects, can assess bat activity over large areas and is now widely used for surveying bats. We have been making car-based mobile transects in the Delaware Water Gap National Recreation Area (DEWA) in Pennsylvania and New Jersey since 2013. Echolocation calls recorded along these mobile transects are identified to species using the SonoBat 3 autoclassifier and then mapped along the transect route using GIS and the program TransectPro. Our past work has assessed post-WNS activity levels and distributions for bat species in DEWA. The present study uses transect data to assess bat habitat preferences and develop species distribution models. We used vegetation data layers in GIS to compare the vegetation types where different species were recorded along our transects. We then produced a MaxEnt model in R to develop species distribution models for bats within DEWA. We found significant habitat preferences for big brown bats (Eptesicus fuscus), eastern red bats (Lasiurus borealis), hoary bats (Lasiurus cinereus), and silver-haired bats (Lasionycteris noctivagans). Low detection rates precluded the development of distribution models for tri-colored bats (Perimyotis subflavus) and for species in the genus Myotis. Future transects that pass through a greater variety of habitat types should increase the applicability of these models. (128)

**Burton, Micah\*, Akeisha Belgrave, and Rachel Fogle** Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Identifying the effectiveness of plant extracts for treating biofilms of <u>E. coli</u> and <u>M. xanthus</u>. — Identifying the effectiveness of plant extracts for treating biofilms of <u>Escherichia coli</u> and <u>Myxococcus xanthus</u> – One of the key factors contributing to antibiotic resistance is the ability for some bacteria to form biofilms. Biofilms are masses of bacterial cells on a surface which are housed in a matrix of polysaccharides. Biofilms can adhere to surfaces in hospitals, and can become resistant to even the harshest disinfectants. Sufferers of the genetic disease known as cystic fibrosis are vulnerable to bacterial infections in the airways of the* 

lungs. The thickened mucus caused by this disease allows for the bacterium *P. aeruginosa* to form biofilms more easily. This allows this bacterial pathogen to linger in the airways of the lungs of these patients causing chronic lung infections, inflammation and possible lung failure. The magnitude of this rising problem elicits a need for novel treatments regarding biofilm-associated infections. There has been a growing interest in the use of plant extracts as a substitute for antibiotics in combating bacteria. Two such extracts include garlic and ginseng which have been shown to clear *P. aeruginosa* biofilms *in vivo* and *in vitro*. To identify a possible broad-spectrum treatment for biofilm-related infections, *E. coli* and *M. xanthus* biofilms were treated with garlic and ginseng oil and bacterial growth and biofilm formation were monitored using spectrophotometry and live imaging techniques. (5)

Byne, Ahana\*, Seema Bharathan, and Narayanswamy Bharathan Indiana University of Pennsylvania, Indiana, PA 15705. Characterization and Protein Profiling of Viral Infected and Noninfected <u>Rhizoctonia</u> solani isolates. — Rhizoctonia solani is a soil-borne plant pathogenic fungus causing important diseases in cultivated crop plants. R. solani is a complex species recognized by its ability to anastomose. Till today 14 anastomosis groups (AG's) have been recognized. Many isolates of R. solani have been recognized. Many isolates of R. solani exhibit varying degree of pathogenicity on the host they infect. Many researches focus on two isolates Rhs 1AP and Rhs 123E that are virulent and a-virulent, respectively. Both the isolates belong to AG-3 with Rhs 1AP containing 2.9 kb double stranded (ds) RNA that is lacking in Rhs 123E. The quantitative alteration of protein was investigated using a combination of protein identification tools such as Polyacrylamide gel electrophoresis (SDS-PAGE), protein chip, 2D-Gel and mass spectrophotometry that helped to compare protein from the selected isolates. SDS-PAGE and protein chip analysis were conducted to isolate total protein and to determine its concentration. Rhs 123E have band size of 30 kDa, 25kDa, 15kDa and 10kDa whereas Rhs 1AP showed band size of 78kDa, 58kDa, 48kDa and 20kDa. Unique protein bands were observed in Rhs 1AP of 48kDa and 78kDa that were absent in Rhs 123E. Additional experiments are being conducted using 2D-DIGE and mass spectrophotometry to develop peptide maps of the unique protein. (85)

Cabrera Vicens, Brenda\*, Kelly Perri, and Joyce Belcher Cabrini University, Radnor, PA 19087. Modulatory effects of prolactin on osteoblasts and chondrocytes in vitro. - In this study, the effects of the hormone prolactin (PRL) were investigated on the formation of bone by osteoblast cells and the formation of cartilage or bone by chondrocytes. The formation of bone is crucial for maintaining a proper posture, and if obstructed, bones are more likely to become brittle. Cartilage functions to insulate bones and prevent any damage to it. Bone disorders, such as osteoporosis, are very common, and it is important to understand bone disorders on the cellular level. There is very little knowledge about how PRL affects bones on the cellular level and if it has a role in bone disorders. It was hypothesized that osteoblast and chondrocyte proliferation and differentiation would increase as levels of PRL increased. In this experiment, different dosages of prolactin were administered to three different groups for each type of cell: a control group, a low dosage group, and a high dosage group. These dosages were intended to mimic real-life physiological events in humans. The model that was followed consisted of 21 days, with critical points on day 7, 14, and 21. Both types of cells used the same model, and different assay and stains were administered or performed on those days. The different assays and stains were proliferation assay, alkaline phosphatase assay, mineralization stains (Alizarin red and Von Kossa), calcium measurement assay, and Safranin O staining. Overall results were that as PRL concentration increased, so did osteoblast and chondrocyte proliferation, while osteoblast differentiation increased, and chondrocyte differentiation was not affected. In conclusion, this study showed the relationship PRL has with osteoblasts and chondrocytes, and it provided a better understanding of PRL for future therapeutic approaches. More research will be conducted on other types of bone cells, such as osteocytes, and osteoclasts. (66)

Callerame, Deanna\* Mercyhurst University, Erie, PA 16546, 6XHis-Tag DNA polymerase-TEVgreen fluorescent protein fusion protein overexpression and purification. — The polymerase chain reaction (PCR) has been a commonly-used technique since it was invented in the 1980s.<sup>1</sup> Although it is a basic laboratory procedure, there are a multitude of projects that involve the amplification of DNA for use in molecular biology, forensics, and so on. Tag DNA polymerase, the enzyme used to synthesize DNA in a PCR, is the most expensive reagent in this reaction and can be created inhouse to save money. By creating a 6XHis-Taq-TEV-GFP fusion protein, the desired product can be visually tracked throughout the protein purification process (immobilized metal affinity chromatography) by the fluorescence of GFP. The TEV sequence between Tag and GFP allows for optional cleavage (by the addition of TEV protease) of the two proteins, Tag and GFP, to compare the polymerase activity of the Tag-GFP fusion Tag alone following purification. The cloning process begins with the modification of pAKTag to remove the natural Tag stop codon and two additional in-frame stop codons down stream. Next, a 6XHIS construct will be inserted into a unique EcoRI restriction site at the N-terminus of the Tag cDNA. Finally, TEV-EGFP will be amplified from the EGFP-pBAD plasmid by PCR. These sequences are then cloned into the modified pAKTag plasmid followed by transformation into E. coli for protein overexpression. Expression of the fusion construct will be induced by IPTG treatment. Three batches of product are assayed by PCR: purified product, un-purified product with added TEV protease, and re-purified product after added TEV protease. The goal is to maintain functionality of Tag DNA polymerase throughout protein purification and overexpression and utilize the visual properties of GFP to track the location of the desired protein in each step of the process. (54)

Campbell, J. Michael\*, John Otto Campbell, Angelea Belfiore, and Harry Rick Diz Mercyhurst University, Erie, PA 16546. A regional perspective on lake cyanobacteria blooms in the PA-NY Lake *Erie region during summer 2017.* – A regional survey was conducted of cyanobacteria blooms occurring during late July 2017 in ten different lakes in the PA-NY Lake Erie region. Publicly accessible locations along the shore of nine of the lakes were sampled with a 5-m long horizontal tow of a 65-micron mesh Wisconsin-style plankton net. Lake Erie's Presque Isle Bay was sampled using 5-m long vertical tows from a boat at mid-bay. The highest total cyanobacteria colony densities, exceeding 200,000/L, were found in Findley Lake, with Chautaugua Lake at Long Point ranking second (189,127/L) and Edinboro Lake ranking third (113,365/L). The lowest late-July cyanobacteria colony densities were found in Canadohta Lake (219/L) and Conneaut Lake (3,751/L). Cyanobacteria densities in Presque Isle Bay in late July 2017 (7,331/L) ranked sixth among the region's lakes, between Pymatuning Lake (8,827/L) and Lake LeBoeuf (6,079/L) sampled the same week. At least one or two cyanobacteria species in the genus Anabaena were found in each of the ten lakes. Aphanizomenon was detected in all of the lakes in late July except LeBoeuf and Canadohta. Microcystis, the genus known for producing microcystin toxin, was found in all of the lakes except Lake LeBoeuf. Highest densities of this taxon were found in Presque Isle Bay (6,740/L), Chautauqua Lake at Long Point (5,313/L) and Eaton Reservoir (3,678/L). Ranking regional lakes' cyanobacteria blooms based upon single-date sampling is not entirely reliable, since we observed a remarkable bloom of Aphanizomenon develop in Lake Pleasant between July 27 (3,978/L) and August 10 (101,538/L). (132)

**Campbell, John\*** Mercyhurst University, Erie, PA 16546. *Toxic cyanobacteria blooms and associated relationship to rotifer population dynamics in Lake Erie's Presque Isle Bay.* — In freshwater pelagic algal communities, responses to nutrient intakes can be seen through changes in population densities, and what organisms are detected in those circumstances. As a continuation of research conducted on Presque Isle Bay from May to October 2016, this study looked at the algal communities in Presque Isle Bay from May to September 2017, enumerating all phytoplankton and zooplankton within the vertical triplicate samples collected by a Wisconsian style 65-micron plankton net. These samples were collected every two weeks from three locations along the midline of the Bay. As part of the two-year study, I examined parallels to environmental conditions and

aquatic biota responses between the same months in 2016 and then of 2017. Over the course of the two-year study, the numbers and presence of the rotifer *Polyarthra* appeared to correlate with cyanobacteria blooms. In this analysis, I focused in from the broad perspective of the whole planktonic community in Presque Isle Bay to try to discern the nature of the relationship between cyanobacteria blooms and *Polyarthra*, with the intent to better understand how these animals manage to maintain large populations in the presence of potentially high levels of cyanobacteria toxins. (**133**)

Campbell, Karen, and Stephen Mech\* Albright College, Reading, PA 19604. The importance of multiple methodologies to survey tropical bat communities. — We surveyed the bat community at Albright's property in southwest Costa Rica, near Corcovado, in January 2018. Over six nights and seven days, we captured 28 bats representing nine genera using a combination of single-tier mist nets (19 individuals) and vegetation surveys (8 individuals). Most of these bats (19/27) were in the family Phyllostomidae, and the others were Thyropteridae (6), Mormoopidae (1) and Vespertilionidae (1). While mist-netting, we performed simultaneous acoustic surveys using a handheld Echo Meter Touch ultrasonic receiver. Recordings revealed a very different bat community, as none of the Phyllostomidae were detected ultrasonically, whereas representatives from five families of bats were identified based upon characteristics of their echolocation signals. Bats in the families Emballonuridae, Molossidae, Mormoopidae, Noctilionidae, and Vespertilionidae are all aerial insectivores, not readily captured using single-tier mist nets as they typically fly near the top of the canopy. By contrast, the nets were placed in areas rich with vegetation visited by frugivorous and nectivorous Phyllostomidae, which facilitated their capture. Phyllostomidae are visually-oriented bats that also use echolocation, but their low intensity calls don't readily detect mist-nets placed in areas that are heavily cluttered acoustically, such as the vegetation on which they feed. By contrast, even when aerial insectivores were detected in more narrow fly-ways in which the nets were placed, they easily evaded capture while foraging around the nets. The results of this study emphasize the importance of using multiple techniques to assess the bat community to take advantage of the strengths of different survey methods to form a more comprehensive picture of a complex community. (38)

Can, Marilyn\*, Jeffery Larkin, Cameron Fiss, and Darin McNeil Indiana University of Pennsylvania, Indiana, PA 15705. Prairie Warbler (Setophaga discolor) abundance and associated vegetation characteristics in managed forests of Pennsylvania and New Jersey. - The Prairie Warbler (Setophaga discolor) is a Neotropical migratory songbird that is experiencing population declines. It is suggested that a driver of these declines is loss of breeding habitat: shrubland and early successional forest communities in the eastern United States. Habitat management has the potential to benefit the Prairie Warbler, however limited information exists regarding the breeding ecology of this species. To inform this knowledge gap, we conducted a study in 2017 to 1) determine if the Prairie Warbler uses sites in recently managed deciduous forests of Pennsylvania and northern New Jersey; 2) explore factors driving variation in site occupancy; and 3) understand territory attributes in central Pennsylvania. My analyses of point count data collected across 122 individual timber harvests revealed that cloud cover positively influenced Prairie Warbler detectability, and quadratic grass and forb cover best-predicted Prairie Warbler occupancy. Prairie Warblers were detected at least once in about 43% of the point count surveys, the most abundant ground cover for point count survey locations with Prairie Warblers present were medium sized (1-2 m tall) saplings and shrubs which covered about 66% of the area surveyed. For male Prairie Warblers that we radio-tracked a minimum of two weeks, the average (n=6 males) home range (95% kernel) was 8.34 ha, and the average core territory (50% kernel) was 0.87 ha. There were no significant differences in vegetation characteristics between home ranges and cores territories of the radio tracked Prairie Warblers. Together, this information serves as baseline data to direct future, larger-scale studies of the Prairie Warbler that will ultimately aid in the creation/maintenance of its breeding habitat. (35)

#### Carr, Krista\*, Daniel Morris, Dylan Kutz, Grace O'Malley, Michael Bilger, and Jack

Holt Susquehanna University, Selinsgrove, PA 17870. Comparison of five similar headwater streams in central Pennsylvania during the summer of 2015-2017. — We compared the benthic macroinvertebrate (BMI) communities between the five headwater streams that flow down the north slope of Penns Creek Mountain in the Bald Eagle State Forest of central Pennsylvania through the summers of 2015 to 2017. The five headwater streams, Little Weikert Run, Green Gap Run, Lick Run, Coral Run, and Henstep Run were similar in size and substrate (sand, cobble, and boulder) and maintained flow even through the drought conditions of 2016. Alkalinity averaged 69.01, 181.21, 187.27, 189.71, and 114.98 microequivalents/L during the three year study for each of the headwater streams, respectively. They were also similar in conductance averaging 17, 24, 21, 22, and 20 microsiemens/cm, respectively. The %EPT (Ephemeroptera, Plecoptera, Trichoptera), for the five headwaters ranged from 23-67% during the entire study period, which, given the sites, was unexpectedly low. We collected the BMI during the first half of July using the 6-kick method, and processed them by the PA DEP and US EPA protocols. When comparing communities at the same sites across the years, the Proportional Bray-Curtis Similarity Index ranged from 19-57% community overlap, which was very low to moderate. During the summer of 2017 the two most similar streams were Green Gap and Coral Run (64% overlap), but all stream community comparisons were moderate to high. During the course of this study we collected 46 taxa across the five headwaters with Crambidae and Empididae being the most dominant making up more than 10% of the total count each. Based on the collections from the summer of 2017 the five streams, though very similar in abiotic parameters, were only moderate replicates of each other as far as the BMI communities are concerned. (139)

Carson, Emily\*, and Dr. Jeffrey Newman Lycoming College, Williamsport, PA 17701. The identification of a novel species and novel genus in the family Bacillaceae. - A bacterial strain was isolated from Loyalsock Creek in January 2016. During an undergraduate microbiology course, the strain was putatively identified as a novel species within the family Bacillaceae. The strain, designated EAC, was found to be closely related to Bacillus luciferensis, Bacillus acidiceler, and Bacillus solisilvae, with 16s rRNA gene sequence similarities of 98.86%, 98.73%, and 99.33% respectively. The phenotypic comparisons observed after Fatty Acid Methyl Ester analysis, Biolog GEN III, and unique gene content analysis showed that *Bacillus sp.* EAC had more similarities to Bacillus luciferensis and Bacillus acidiceler than to Bacillus subtilis, the Bacillus type species. The average amino acid identity (AAI) between Bacillus sp. EAC and the reference organisms, Bacillus luciferensis, Bacillus acidiceler, and Bacillus solisilvae, was between 82%-83%. These values fall below the 95% species threshold. The average amino acid identity when comparing the three reference strains or Bacillus sp. EAC with Bacillus subtilis was 56%. This is less than the 70-95% similarity observed among organisms in the same genus. These results suggest that that these four organisms belong in a different genus than Bacillus subtilis. Many other species in the family Bacillaceae have been misclassified into the genus Bacillus and later moved into new genera. As such, Bacillus sp. EAC, Bacillus luciferensis, Bacillus acidiceler, and Bacillus solisilvae may belong in a novel genus within Bacillaceae. (17)

#### Chetlin, Robert, Shannon Farbacher\*, Callie Paddock\*, Ryan Riemedio, and Bradley

**Jacobson** Mercyhurst University, Erie, PA 16546. *Postural performance, neurocognition, and selfreported concussion: a prospective longitudinal study of incoming Division II collegiate freshmen football players.* — We previously reported an inverse relationship between number of self-reported concussions and multiple measures of postural stability in one group of incoming asymptomatic Division II freshmen football players, while ImPACT scores demonstrated no relationship to prior self-reported concussion number. Postural stability deficit following acute sport-related concussion is well-documented. Potential latent effects on postural performance in newly matriculating, asymptomatic, freshmen collegiate football players have not been examined in longitudinal fashion. **Purpose:** To determine the relationship between agility, postural stability, neurocognitive

measures, and self-reported concussion in three different groups (re: by year) of Division II freshmen football players, prior to beginning their collegiate careers, and; to examine differences in these outcomes by position group. Hypotheses: We hypothesize that: (1) additional differences in bilateral agility and postural stability scores will be found between multiple position groups, and; (2) inverse relationships will be revealed for single-leg and double-leg postural stability measures and number of self-reported concussions. Methods: Seventy-eight Division II freshmen football players, across three different academic years (2015-2016, n=25; 2016-2017, n=21; 2017, n=32), participated in offseason testing: agility was measured using a 20-yard shuttle run; postural stability was assessed with the BIODEX Balance System, and; neurocognitive function was evaluated with the ImPACT inventory. Self-reported concussion occurred at least six months post-insult. 1-way ANOVA will be used to compare performance and neurocognitive outcomes between the three freshmen classes. Pearson-product moment correlations will be used to examine relationships between variables. Players will be grouped by position for further statistical analysis: lineman/linebackers (L/LB, n = 36); running backs (RB, n = 10); wide receivers/defensive backs (WR/DB, n = 23), and; guarterbacks/kickers (QB/K, n = 9). Multivariate pairwise comparisons will be used to evaluate differences between position groups. Statistical significance will be set at p<0.05. (96)

Childs, Amanda B.\*, and Lindsey A. Welch Cedar Crest College, Allentown, PA 18104. The effect of chain length on kinetics and thermodynamics in the esterification of model compounds present in biooil. - Renewable and alternative energy sources are becoming an immediate need due to the over-depletion of petroleum and fossil fuel reserves, rising CO<sub>2</sub> emissions, and associated climate change. Biooil from pyrolyzed hard wood contains many organic compounds, such as carboxylic acids, that can be converted into esters by esterification with the use of a solid acid catalyst. Esters can be used as a biofuel that is sustainable and renewable. Propionic acid and valeric acid, model compounds in biooil, were reacted in ethanol with a sulfated silica solid acid catalyst. Reactions were carried out at 40°C, 50°C, 60°C, and 70°C at ambient pressure. Progress was monitored with the analysis of products using gas chromatography mass spectrometry. Kinetic and thermodynamic data were collected and used to construct Arrhenius and Eyring plots. By varying temperature and the carbon length of the starting compound the energy of activation and rate of the production of the corresponding esters were studied. The effect of chain length on kinetic and thermodynamic data will be presented. Current results show that a shorter chain length increases the initial rate of reaction. These results could help optimize conditions used to produce fuel grade chemicals. (173)

**Cirilo, Joseph\*, and Julie Belanger** Kings College, Wilkes-Barre, PA 18711. *The effect of "Ouzo-like" colloids containing N-phenyl-1-naphthylamine on the survivability of SHSY-5Y Cells in vitro.* — Drug delivery systems using vesicles and suspensions, are currently in research for many different diseases. This study aimed to investigate the effects of a specific suspension, an "Ouzo-like" derived colloid, on the survivability of SHSY-5Y cells (a neuroblastoma cell line). The colloid used in this study was formed of N-phenyl-1-naphthylamine (NPN) dissolved in dimethylsulfoxide (DMSO) and suspended in phosphate buffered saline (PBS). The cells were treated with either a complete media negative control, retinoic acid positive control (routinely used to induce differentiation), or one of two colloid treatments for 24 hours at 37°C in 5% CO2. A survivability assay using Presto-Blue showed no statistically significant difference across treatments, suggesting that the colloids did not affect the survival of the cells. This implies that further research into the effectiveness of the system regarding the integration of retinoic acid would be beneficial, as well as membrane staining to track the fluorophore, NPN, as it is integrated into the cells. (161)

#### Clark, Kyle \*, and Jana Villemain Indiana University of Pennsylvania, Indiana, PA

15705. *Characterizing Protein Interactions and Conformation Changes of the* <u>S. cerevisiae</u> Srs2 *Helicase C-terminal Domain.* — We are investigating the possibility that the *S. cerevisiae* Srs2 helicase C-terminal domain (CTD) undergoes conformational changes triggered by interactions with

different proteins and phosphorylation to toggle its function based on cellular conditions. The Srs2 helicase CTD interacts with multiple proteins involved in the DNA damage response and is known to remove Rad51 recombinase from DNA via a direct protein interaction to regulate homologous recombination (HR). Upon detection of DNA damage, the Srs2 CTD is phosphorylated and its activity altered to allow initiation of HR. Our analysis of the Srs2 CTD amino acid sequence indicates that this protein region shares little sequence homology with other proteins, but harbors many features common to known intrinsically disordered proteins. These proteins are noted for adopting different structures with altered functions based on protein interactions or modifications. To begin examining the Srs2 CTD structure and conformation changes, we overexpressed an Srs2 CTD protein fragment corresponding to amino acids 783-1174 with an N-terminal His-tag and isolated it from *E.coli*. We show here that the Srs2 CTD protein fragment isolated in our lab interacts with the Rad51 recombinase in vitro as reported previously for the 783-1174 CTD fragment examined by yeast two-hybrid analysis. Comparison studies were carried out with the fulllength Srs2 helicase and bovine serum albumin to serve as negative-interaction control. Studies are also underway to detect and monitor conformational changes in the Srs2 CTD in the presence and absence of the Rad51 protein using fluorescence spectroscopy with the single Trp 812 in the fragment serving as a probe reporting on changes in its environment. Chemical modification of Cys1020 in the Srs2 CTD with a fluorophore can provide additional information on protein conformation changes due to interactions with Rad51 through fluorescence resonance energy transfer studies. (104)

Clarke, Justin\*, and Terry Master East Stroudsburg University, East Stroudsburg, PA 18301. The Northern Waterthrush: analyzing the distribution and abundance of a secretive songbird in Pennsylvania. - Northern Waterthrush (Parkesia noveboracensis) (NOWA) showed a drastic decline between the first and second Pennsylvania Breeding Bird Atlas (PBBA) efforts. This is one of the largest declines of any Pennsylvania breeding species in the ~20 years between the two atlas periods. This decline is especially concerning because, while all of the blocks were surveyed in the first atlas, the effort was more extensive in the second atlas. During the second PBBA, data suggested a slight northward range contraction and perhaps a more noticeable increase in elevation of occupied blocks, both trends implicating climate change as an influence on the population. This study further refines the distribution shown in the latest atlas effort and investigates potential factors that may be responsible for detected changes in distribution. In the spring of 2017, extensive wetland surveys were conducted in Northampton, Monroe, and Pike counties in Pennsylvania for singing males. At each of the 12 occupied sites found, two point counts were conducted to characterize the avian community in NOWA habitat. Measurements on vegetation structure/composition and hydrology were also collected. These data characterizing occupied NOWA habitat will be compared to currently unoccupied sites where individuals were detected either during the 2<sup>nd</sup> PBBA or sites with suitable habitat where no individuals were detected during our own targeted wetland surveys. In the process of conducting this study, natural history data/observations will also be collected including data on reproductive behavior which is lacking in Pennsylvania. (64)

**Cook, Ryan\*, Arie Van Wieren\*, and Sudipta Majumdar** Indiana University of Pennsylvania, Indiana, PA 15705. *Application of Bacterial Adenylate Cyclase Two Hybrid (BACTH) system for studying alanine racemase dimerization in vivo.* — The burden of antimicrobial resistance (AMR) is manifest in the reemergence of previously well-managed infectious bacterium including *Mycobacterium tuberculosis* (MT) and *Streptococcus pneumonia* (SP). The urgency with which new approaches to infection mitigation must be explored is a function of the increasing worldwide death toll and economic strain associated with infection by AMR bacterium such as MT and SP. Alanine racemase (Alr), a catalyst that is responsible for supplying a necessary precursor for bacterial cell wall biosynthesis, is one potentially potent antibacterial objective that has not yet been fully explored. Alr has several structural components necessary for efficient functioning that have been identified but not thoroughly investigated as possible targets to disable the enzyme. One structural target is exploitative of the fact that monomeric Alr cannot effectively isomerize its substrate, i.e. Alr must dimerize in order to function. Disrupting dimerization would effectively inhibit the enzyme and result in death of the bacteria. A system to assay dimerization (or absence thereof) must be developed in order that the effectiveness of disruptive agents may be assayed. The dimerization of Alr from MT and SP were examined using the bacterial adenylate cyclase two-hybrid (BACTH) system. The Alr gene from MT and SP were amplified using PCR and then cloned into the expression vectors pKT25 and pUT18c by genetic recombination. Recombinant plasmids were co-transformed into *E. coli* and dimerization was qualitatively measured using colorimetric assay on MacConkey/maltose agar and X-Gal/IPTG plates. (92)

Corpus, Larry\* Misericordia University, Dallas, PA 18612. Mayfly (Insecta: Ephemeroptera) fauna of the upper Meadows Pond, Dallas, PA. – The potential use of aquatic macro-invertebrates as bioindicators of water quality in streams is well known, with metrics like the EPT index that uses numbers, species, and tolerance values of Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies) to determine a value. While the EPT index may be appropriate for streams, the use of such metrics to assess the water quality of ponds with higher water temperatures, greater pollution, lower oxygen levels, and fewer indicator species may be guestionable. Developing baseline species lists for multiple ponds may represent a partial answer to biological assessment of lentic waters by comparing species commonalities from different pond habitats. The upper Meadows Pond (uMP) was the first pond to be sampled for this purpose. Sampling was initiated in the uMP in June 2016 and continued through May 2017. Specimen samples were collected monthly by aquatic sweep net from the vegetated and non-vegetated littoral region in order to determine what organisms might occur in the littoral zone throughout the year. The diversity, abundance, and habitat preferences of the Ephemeroptera in the uMP are reported on here. A total of 1,049 mayflies were collected, currently constituting three families and four genera, including the Baetidae: Baetis sp.; Ephemerellidae: Eurylophella sp. and Drunella sp.; and Tricorythidae: Tricorythodes sp. The majority of the mayfly nymphs were collected from vegetated sites, suggesting that there may be an association with the aguatic macrophytes along the shoreline. Baetis, Eurylophella, and Tricorythodes nymphs are considered collector-gatherers, while Drunella varies from a scraper as a young nymph to become a predator as a more mature nymph. Major morphological character differences among the different mayfly species were documented using microphotographic techniques. (136)

Culichia, Fernanda\*, Alexis Zigarelli\*, Jean-Francois Therrien, and Allison Cornell Cedar Crest College, Allentown, PA 18104. Diet composition and variation; possible correlations to American kestrel (Falco sparverius) reproductive output. — A decline in the American kestrel (Falco sparverius) population in the Northeastern part of North America has been observed since the mid-1984. The reasons for this ongoing decline are still being assessed. In this research project, we tested a connection between diet variation and fecundity. Across its range, the American kestrels' main prey source seems to be small mammals, though they also eat different invertebrates. We predicted that nests with higher vertebrate prey numbers would yield a higher number of fledged chicks since vertebrates, compared to mass and size of invertebrates, provide more energy to the kestrels. We examined regurgitated materials from nesting kestrels around Hawk Mountain (PA) to determine their diet composition. Pellets collected at 28 nest boxes from 2012-2017 were analyzed. We assessed vertebrate and invertebrate ratios in the diet and compare these ratios to the number of chicks fledged from nests using linear regression models. We found no relationship between the ratio of vertebrate prey in a nest and the number of chicks fledged suggesting that the ratio of vertebrate prey in the American kestrel diet does not correlate with the number of chicks fledged. (29)

**Curry, Adam** Penn State University Wilkes-Barre, Lehman, PA 18627. *Does caffeine cause cannibalism? A test in <u>Tenebrio molitor</u>. — Caffeine is a plant defense chemical that functions as an insecticide. As humans increase their consumption of caffeine there is a corresponding increase in environmental caffeine exposure for aquatic and terrestrial species. While it functions as a stimulant and appetite suppressant for humans, this chemical has varied effects in insects ranging from improved memory (at low doses in flower nectar) to reduced growth, limited reproduction, and death. We tested the effects of caffeine exposure on growth, reproduction, survival, and rates of cannibalism in the darkling beetle, <i>Tenebrio molitor*, over a period of 20 weeks. We expected to find slower growth rates in the caffeine exposed colonies and higher rates of cannibalism as a consequence of increased metabolic activity. Surprisingly, the control colonies exhibited cannibalistic behavior sooner than caffeine-exposed colonies, and the pupal life stage was significantly decreased in the control colonies, likely as a result of cannibalism from adult beetles. These results suggest that caffeine may function as an appetite suppressant in this species, thereby reducing the rate of cannibalism. **(63)** 

Daniel, Karis\*, M. Dana Harriger, and Budhan Pukazhenthi Wilson College, Chambersburg, PA 17201. Validating fecal DNA technologies for ungulate conservation. — The use of fecal DNA as a tool for ungulate conservation has been validated for several threatened species, but with mixed success. Degradation and low DNA concentrations challenge its reliability for use in genomic research. This study assessed validity and integrity of fecal DNA for two critically endangered ungulate species. Over six weeks, DNA was collected, isolated, and analyzed from fecal samples of Scimitar-horned oryx (Oryx dammah dammah, n=7) and Dama gazelle (Nanger dama ruficollis, n=4) at the Smithsonian Conservation Biology Institute. One set of fecal samples was processed fresh; two additional sets were incubated (40 °C) to simulate effects of heat degradation. DNA was isolated from all samples using QIAGEN's MO BIO PowerFecal© DNA isolation kit, and sample purity for all three treatments (fresh, 24h, 1 week) was tested using a NanoDrop<sup>™</sup> Spectrophotometer. DNA quality was analyzed using PCR and gel electrophoresis to amplify two primers: Cytochrome-b (421bp) and a control region fragment (560bp). DNA isolated from fecal samples was of sufficient purity for utilization in further analyses. There was no significant difference between DNA purity in fresh or incubated treatments for either O. dammah dammah or N. dama ruficollis. Fragment amplification was successful for both species. Cytochrome-b produced stronger amplification of O. dammah dammah DNA, while the control region fragment proved slightly more effective with N. dama ruficollis DNA. These results suggest that species-specific genomic DNA can be isolated from O. dammah dammah and N. dama ruficollis fecal samples (Cytochrome-b and control region), and short-term heat exposure does not necessarily undermine the utility of this DNA for genomic analyses. (129)

**Darok, Matthew\*, and John Harms** Messiah College, Mechanicsburg, PA 17055. *In vivo effects of proglumide treatment on pancreatic tumor growth and fibrosis. — In vivo* effects of proglumide treatment on pancreatic tumor growth and fibrosis — Pancreatic cancer is an incredibly lethal disease, as it is currently the fourth most common cause of cancer-related death in the United States. Nearly three-quarters of patients will not survive longer than a year past initial diagnosis, mainly due to the fact that traditional cancer treatments are generally ineffective and do not improve one's prognosis. It has been suspected that the ineffectiveness of chemotherapy is due to the highly fibrotic nature of the pancreatic tumor microenvironment, which reduces blood flow and drug delivery to the tumor. Gastrin, a gastrointestinal hormone, has been shown to contribute to the proliferation of pancreatic cancer cells, and preliminary evidence suggests that it also plays a role in this increased fibrosis. In order to study the effects of gastrin signaling on the tumor stoma, mice (C57BL/6) were injected orthotopically with Panc02 pancreatic cancer cells and randomized to treatment with proglumide (a gastrin antagonist; n=7) or control (n=6). Tumor growth was monitored for 4 weeks and following necropsy, tumors were quantified for fibrosis via Masson's trichrome staining and Second Harmonic Generation (SHG). Fibrotic volume in the tumor microenvironment

was significantly decreased with proglumide treatment, although no significant difference in tumor mass was observed. Studies to quantify changes in vascularization, immune cell infiltrate, and sensitivity to concurrent chemotherapy are ongoing. (**112**)

Dea, Stephanie\*, and Stephen Mech Albright College, Reading, PA 19604. Effects of ectoparasites on survivorship and reproduction of Peromyscus leucopus. - White-footed mice (Peromyscus leucopus) are important members of the forest community for seed dispersal and as potential prey items. These mice are frequently parasitized by botflies (Cuterebra fontinella), fleas (Order Siphonaptera), and ticks (Ixodes scapularis). The effects of botflies on P. leucopus range from minimal effects to increased survivorship, and there is no evidence of fleas or ticks affecting mouse survivorship. There is, however, evidence of increased botfly parasitism on white-footed mice near woodland edge. Because the habitat in logged areas resembles the forest edge habitat. mice in logged areas may have higher infestation of bot flies. We examined the effect of ectoparasite load on survivorship and other population demographics of white-footed mice in a managed forest near Reading, PA. We tested three hypotheses: 1) mice with greater numbers of parasites will have reduced cues of reproductive ability (e.g., pregnancy rates, lactation, and scrotal size); 2) the frequency of infestation will be greater in the site that was selectively logged to improve forest health than the control site, which was unaffected by any logging. We used mark-recapture and  $\chi^2$  analyses to test our hypotheses. Survivorship increased in both habitats over the course of the summer trapping period. The proportion of infected and uninfected individuals was the same on each site despite statistically different population densities. Mass was unaffected by infection status, but infection was influenced by age on the select cut site, but not the control site. These relationships should be investigated further. (126)

Deak, Michael\*, and Scott McKenzie Mercyhurst University, Erie, PA 16546. Inferences on tyrannosaurid social behavior based on enigmatic maxillary depressions and distribution of neurovascular foramina. - Tyrannosaurids are among some of the most famous and diverse clades of coelurosaurian theropods. A new taxon was described from the Two Medicine Formation in Montana (Carr et. al. 2017), and was suggested to possess highly sensitive head scales due to the texture of the facial bones similar to those found in crocodilians. Hypersensitivity in theropod snouts has also been proposed for various other taxa such as Spinosaurus (Ibrahim et. al. 2014) and Neovenator (Barker et. al. 2017). Tyrannosaurids are unique in this case as they possess various depressions in their maxillae as well as a wide variety of foramen. Previous examinations claimed that these depressions were pathologies sustained via intraspecific combat (Rothschild et. al. 2008 and 2013, Hone et. al. 2015). The size of the depressions relative to the thickness of a taxon's tooth supports the latter hypothesis. Juvenile tyrannosaurids of various taxa also have a relatively smooth texture of their facial bones, which is contrary to what is seen in crocodilians (Milinkovitch et. al. 2013). However, this does not disprove the possibility that tyrannosaurids had hypersensitive snouts as it could possibly explain why the facial regions were popular targets during agonistic face biting displays. In terms of Tyrannosaurus rex, maxillary depressions are predominantly seen in the gracile morphotype and are lacking in the robust morphotype, which could be further evidence for sexual dimorphism in that taxon (Larson 2008). Robust morphotypes also poses a higher foramen count than the smaller gracile morphotypes. Maxillary depressions show that tyrannosaurids fought with each other to fight for mates, and hypersensitivity could be a reason why the head was such a popular target. Given that females have a higher than males, and that various foramen patters exist in individuals of various taxa, face rubbing could have been a common greeting gesture in tyrannosaurids. (123)

**DiPippa, Cassandra\*, and Barbara McCraith** Misericordia University, Dallas, PA 18612. *A survey of caddisfly larvae (Order Trichoptera) in two northeastern Pennsylvania streams.* — The relationship between community structure and habitat function is an important ecological subject. By monitoring the biodiversity and abundance of certain benthic macroinvertebrate groups, one can better understand stream health. The diversity and sensitivity to changes in water quality of

caddisfly larvae (Order Trichoptera) makes them an ideal organism for use as a bioindicator of stream health. The purpose of this study was to survey the diversity and abundance of Trichoptera in both Leonard Creek, Wyoming County, and Trout Brook, Luzerne County, Pennsylvania. I hypothesized that there will be no significant difference in trichopteran abundance and diversity between the two study sites. This research spanned ten months, beginning in February of 2017 and ending in December of 2017. This is a part of an ongoing long-term study and preliminary results suggest that trichopteran diversity has decreased since the study began in 2012. The data gathered could potentially be used in future studies regarding stream health. (**145**)

Doran, Taylor\*, and Andre Walther Cedar Crest College, Allentown, PA 18104. Identification of genetic markers to rapidly genotype strains of yeast used in beer production. — Beer making involves the fermentation of sugars extracted from malted grains using different species of brewing yeasts. There are many species of brewing yeasts used in beer production, but two of the most commonly used are the top fermenting yeasts species Saccharomyces cerevisiae used in the brewing of ales, and the bottom fermenting yeasts species Saccharomyces pastorianus used in the brewing of lagers. Different yeast strains lead to different flavors, alcohol contents, and color profiles, so it is important to use monocultures of the proper yeast strain to obtain the desired beer. Contamination of fermentation tanks by other brewing strains or wild yeast strains not normally used in the brewing process can lead to undesirable beer outcomes. The problem of contamination is particularly relevant in large breweries that use fermentation tanks for different kinds of beers. Current methods to identify yeast contamination use biochemical and metabolic tests that may take up to a week to obtain results, at which time large volumes of beer may have been tainted by the contaminating yeast. Our research focuses on developing molecular analysis tools to genetically identify beer yeasts using techniques such Short Tandem Repeat PCR with gel analysis and capillary electrophoresis. After analyzing the results of our repeated genomic DNA isolation and identification tests, we have developed a protocol which is more streamlined than any currently available methods available to identify the difference between their beer strains and any contaminants. Thus far, we have identified three loci which we can amplify and use to distinguish different species of beer yeasts. We continue to search for more prominent distinguishing loci that we can use to enhance and further develop our current protocol method for future use by largescale brewers. (24)

Dosch, Brittany\*, and Deanne Dulik Garver Marywood University, Scranton, PA 18509. Use of physical and chemical forensic analysis procedures to characterize fibers found at crime scenes. -While instrumental analysis has come to dominate the forensic science field, some of the most reliable methods of forensic investigation are still wet-chemistry techniques. In the case of forensic fiber analysis, it may be beneficial to rely more on chemical based analytical techniques for fiber analysis and identification. This research evaluated various fibers, both synthetic and natural, to study the accuracy and precision of chemical and physical tests of each fiber as well as use instrumental analysis to compare results. Physical tests of each fiber included burn tests, density tests, microscopy, and hydrostatic weighing, while chemical tests included solubility tests, dyestripping, re-dying using testfabric identification stains (TIS), and thin-layer chromatography. The instrumental analysis that will be performed on each fiber will be infrared spectroscopy in order to identify functional groups within each type of fiber. The results of each test could discriminate natural from synthetic fibers. Once the properties of the known fibers were stablished under our experimental conditions, unknowns were tested in a simulated forensic experiment to determine what type of fiber is present. The impact of these studies and the further research they warrant will be an ongoing study in order to identify the best and most reliable methods of fiber analysis in simulated forensic crime scene experiments. (163)

**Einsig, April\*, and Jessica Nolan** York College of Pennsylvania, York, PA 17405. *The impact of human recreation on the behavior and physiology of aquatic basking turtles at Lake Marburg (Hanover, PA).* — Human recreation in lakes, including fishing and boating, can impact

aquatic turtle populations by changing their behaviors and physiology. The objective of this study was to determine the impact that human recreation had on three turtle species: red-bellied turtles (Pseudemys rubriventris), red-eared sliders (Trachemys scripta elegans), and painted turtles (Chrysemys picta) in Lake Marburg, York County, Pennsylvania. The impact on red-bellied turtles is of particular interest as they are threatened in the state of PA. Turtles were trapped and observed basking to estimate abundance in a given cove. When captured, shell damage and stress hormone levels (corticosterone) were recorded. Data from high-recreation coves, with large amounts of human disturbance, and low-recreation coves, with little or no human disturbance, were compared. Results showed a larger abundance of turtles were captured and recorded basking in high-recreation coves in Lake Marburg. This does not support the original hypothesis that recreation would negatively impact abundance. However, turtles captured in high-recreation coves did suffer more shell and limb damage and had slightly higher levels of stress hormones, although these trends were not significant. Frequent boating and fishing appears to have variable impacts on turtles within Lake Marburg. Activity from boaters and fishers may increase food availability, but also result in more frequent interruption of basking and even occasional injury from boats and fishing hooks. Creating awareness of the aquatic turtle populations through outreach activities, increasing the number of basking platforms and limiting powerboat activity during key times of year may help to insure the longevity of Lake Marburg's turtles. (147)

**Endres, Kodi\*, and Sanda Maicaneanu** Indiana University of Pennsylvania, Indiana, PA 15705. *Assessing raw and treated natural zeolite ability to remove methyl green and toluidine blue dyes from aqueous solutions.* — Kodi Endres and S. Andrada Maicaneanu\* Removal of Toluidine Blue (TB) and Methyl Green (MG) cationic dyes was performed using raw and treated natural zeolite (zeolitic volcanic tuff). Several treatments were applied on the raw zeolite sample (Z): thermal (200-750°C for 2 or 4 hours), chemical (NaCl 1 and 2 M, room temperature and 100°C; HCl 1 and 2 M) and ultrasonic (100 or 180 W, 5-15 min). A FTIR study was also conducted in order to explore how various treatments influence the zeolite structure. Adsorption experiments were performed in batch conditions (25±0.1°C, 100 mg dye/L, 100 mL, 1 g adsorbent) in a precision shaking thermostated water bath (50 rpm). In case of TB adsorption capacity, while for MG adsorption the most efficient sample proved to be the one treated at 500°C for 2 hours with 96% efficiency and 11.88 mg/g adsorption capacity. A down flow mode fixed bed column study was also performed on selected samples in order to highlight the versatility of the chosen adsorbent as an efficient material for dye removal from wastewaters. (3)

Eplett, Sarah\*, and Ryan Colyer Cabrini University, Radnor, PA 19087. A custom fluorescence lifetime spectroscopy system developed with a novel digital circuit. — Optical components, a prototype photon detector, and custom electronics and software are utilized in the development of a custom detection and acquisition system. This microscope uses a laser to excite fluorophores in order to count individual photons using compressive sensing and lifetime imaging. A major component of this project involved the design of a custom electronic circuit using a fieldprogrammable gate array (FPGA) to acquire fluorescence lifetime information for each photon detected. The FPGA circuit design is based on the principle of digitally tagging the arrival time of each photon, providing both nanosecond scale lifetime information and the larger time scale information which will allow photons to be assigned to compressive sensing frames. A custom program has been created in Python to upload the circuit, obtain photon counts from the new hardware, and process the timing information for these photons. Later custom software will be used to reassemble this data into fluorescence lifetime images. A custom detection path has also been developed making use of lenses, mirrors, filters, and a custom photon detector. In order to do so, the circuit board has successfully been connected to the laser and detector. Measurements taken by this system will characterize the response to light intensity levels, and the time response to fluorophores with various fluorescence lifetimes. These will be used to construct phasor plots of the

fluorescence lifetimes to demonstrate the type of data which will be used for the later compressive sensing system. This project is expected to lead to a novel and cost-effective design for efficiently acquiring fluorescence lifetime images under low light conditions which are favorable for biological samples. (2)

Ernesti, Altan\*, Marta Mendez, John Miller, Daniel Morris, Jack Holt, and Michael

Bilger Susquehanna University, Selinsgrove, PA 17870. Benthic macroinvertebrate response to variation in fall discharge of the upper main stem of the Susquehanna River. - The study of benthic macroinvertebrate (BMI) communities allows researchers to analyze the general water quality and habitat health of the streams they inhabit. This study, currently in its ninth year, uses BMI to assess the health and status of the upper main stem of the Susquehanna River in Snyder County, Pennsylvania. Two sampling sites were utilized along the channel to the west of Byers Island, below the Susquehanna's major confluence of the west and north branches. Site 1 is in the West Branch Plume of the river, and is influenced by acidic mine drainage. Site 2, however, is in the North Branch Plume and influenced by agricultural drainage. Three methods were used to sample each of the sites. Following EPA guidelines for sampling non-wadeable streams, rock baskets and Hester-Dendy samplers were deployed as passive sampling methods and captured drifting and colonial BMI. An active kick-sampling method, developed specifically for the Susquehanna River, was also utilized at each site. The results were compared to discharge data gathered by the USGS from their gage in Sunbury, Pennsylvania. Discharge was important to the analysis, due to repeatedly dry fall months in the past three years, and an increase in flow before the end of October. The year 2017 displayed a similar pattern to 2014-2016 with a low discharge rate of 2,000-5,000 cfs, however, the increase in flow (up to 28,000 cfs in previous years) did not occur until late October (discharge reached 70,000 cfs), after the samplers were retrieved. Previous studies observed a drop in Shannon Diversity (1.50 to 1.15), and Bray-Curtis values (91% - 50%) in site 1 between 2015 and 2016, while the Hilsenhoff Biotic Index value rose (3.51 – 5.36), due to the low-flow conditions. Such fluctuations highlight the importance of multi-year sampling of higher order streams, like the Susquehanna. (140)

**Estes, Kiera\*, Alexis Hagelgans , Ty Sampsell, and Avijita Jain** Indiana University of Pennsylvania, Indiana, PA 15705. *Tuning The Photoinduced Ligand Exchange and DNA Interaction Properties of a Series of Ru(II) Monometallic and Ru(II)Pt(II) Bimetallic Complexes.* — Photodynamic Therapy (PDT) is an alternative cancer treatment that is not widely known. Sterically strained Ru(II) complexes have been shown to interact with DNA upon photoirradiation, in the absence of oxygen; a key requirement for an efficient PDT agent. Ru(II)Pt(II) complexes have shown to display multifunctional interactions with DNA upon light activation. Herein, we will report synthesis, characterization, redox properties, spectroscopic properties, photoinduced ligand exchange studies, and DNA interaction studies of a series of six new metal complexes with general formula [Ru(TL)(dpp)]<sup>2+</sup> and [Ru(TL)dppPtCl<sub>2</sub>]<sup>2+</sup> (where TL= 6-Methyl-2,2'-dipyridyl (6-Mebpy), 6,6'-Dimethyl-2,2'-dipyridyl (6-Me<sub>2</sub>bpy), 4,4'-Dimethyl-2,2'-dipyridyl (4-Me<sub>2</sub>bpy), and 2 3-bis(2-pyridyl)pyrazine (dpp). (**165**)

**Farrell, Andrew\*, Keith Gehman, and Derek Straub** Susquehanna University, Selinsgrove, PA 17870. *The effects of buffers on biogas production in anaerobic digesters.* — Anaerobic digestion of organic waste products in a controlled system can solve two problems at once: by transforming waste into a useable product and by producing valuable energy. Anaerobic digestion is the breakdown of organic material in the absence of oxygen. Rather than producing CO<sub>2</sub> and releasing it into the atmosphere as in aerobic decomposition, anaerobic digestion produces methane. By capturing and combusting this methane, energy can be released as heat or turned into electricity. The objective of this study is to evaluate the effect of buffers on methane production during anaerobic digestion. This was done on the lab scale for ease of investigation. Nine 2-liter Erlenmeyer flasks in a heated enclosure were filled with digestate from a large scale anaerobic digester. Three digesters were used as controls without feedstock, three digesters included potato

as a feedstock, and three digesters included potato feedstock and a sodium bicarbonate buffer. The viability of using buffers to maintain an ideal pH and therefore increase methane output was evaluated by measuring the volume of biogas produced and analyzing the methane concentration. Preliminary results from initial experiments have shown significant variability. Results from this new, on-going experiment will be presented. (**170**)

Farrie, Haley\* Saint Vincent College, Latrobe, PA 15650. Natural and social science methods to investigate sources of enteric pathogens in rural Guatemala. - Interdisciplinary approaches are essential to solving complex problems in developing countries. In Guatemala, diarrheal disease is the third leading cause of death for children under the age of five. Children suffering from reoccurring diarrheal infections and chronic malnutrition have weakened immune systems, stunted growth, and reduced intellectual and work capacity as adults. This study emerged from the needs of the local community partner, the Organization for the Development of the Indigenous Maya (ODIM), and utilized methods from both Biology and Anthropology to investigate the sources of enteric pathogens in two towns. Presence-absence field tests were used to measure fecal indicators in flies, and revealed that 100 percent of samples were contaminated with Hydrogen Sulfide Producing Bacteria (HSPB) and Escherichia coli. Rapid assays were used to measure parasites in 21 samples of dog feces. 70 percent of fecal samples collected were infected with Giardia and 40 percent of samples were infected with Cryptosporidium. These results were substantially higher than baselines in other South American countries, and indicate a potentially high prevalence of these pathogens in the local dog population. Other studies show a burden of Giardia and Cryptosporidium in the human population. These results may be used to initiate a local public health campaign to routinely treat the dog population for parasites in an effort to reduce the presence of parasites in the environment. Semi-structured interviews were conducted with 30 local mothers to assess sanitation practices and the receptiveness to new interventions. Respondents often reported practicing proper home sanitation techniques but desired more effective control of flies and animals in the local environment. This study shows the importance of using molecular methods in combination with qualitative methods. Future studies may focus on research dissemination, implementation of additional sanitation interventions, and monitoring the effects of routinely treating the dog population for parasites. (154)

Fischer, Katie\*, Tanya Matlaga, and David Matlaga Susquehanna University, Selinsgrove, PA 17870. Effects of native and invasive crayfish chemical stimuli on larval salamander growth. -Nonnative predators have been introduced to many ecological communities, including freshwater streams. Their impact is not fully understood, save for the fact that they facilitate changes in species diversity, abundance, and overall community structure. The invasive predator examined in this study, Orconectes rusticus, or the Rusty crayfish, has been infiltrating rivers and streams in the Susquehanna River watershed, outcompeting and displacing native species of cravfish such as Cambarus bartonii. A shift in predatory crayfish species may impact prey species occupying the same stream. Prey species often avoid chemical cues released by predators, and larval amphibians sometimes undergo life history and morphological changes in response to these predatory cues. One such prey species, the salamander Eurycea bislineata, is found in streams invaded by the Rusty crayfish. This study aims to determine differences in morphological plasticity displayed by larval salamanders in the presence of predatory cues from the invasive crayfish species, as opposed to those given off by the native species. From October to December of 2017, larval salamanders were exposed to regular doses of water containing cues from either C. bartonii, O. rusticus, or neither. Length, width, and head width measurements were taken at the beginning and end of the experiment, and growth rates will be compared. Since the Rusty crayfish is more aggressive than C. bartonii, we hypothesize that larval salamanders will exhibit more significant growth upon prolonged exposure to invasive crayfish chemical cues. Determining changes in a system's dynamics caused by the introduction of a new species is essential for the continued understanding and potential improvement of an impaired watershed. (144)

Frantz, Devin\*, and Jeffrey Newman Lycoming College, Williamsport, PA 17701. Isolating a species of bacteria capable of degrading an unusual carbon source. - Pollution by substances like plastic are becoming a major concern for humanity and the health of the environment. With limited means of removing these pollutants, these substances remain in the environment for large periods of time. A potential solution is through bioremediation with bacteria. Bacteria are a potential solution because of the diversity that exists on Earth. Billions of bacterial species are estimated to live on Earth and most have not been isolated or studied. This could mean that a species capable of degrading a pollutant exists. In the Spring 2017 Microbiology course, bacterial samples were enriched with different pollutants in an attempt to isolate a species capable of degrading a pollutant. From these samples, nine organisms showed interesting growth characteristics when grown in the presence of a pollutant. Of these nine organisms only one would be selected to be the basis of future studies. The selected organism was identified as *Flavobacterium* sp. WLB which grew when enriched with paper. When enriched with paper, F. sp. WLB shows increased growth and has the ability to shred the paper that it is being grown with. Genomic comparisons revealed this organism is actually another novel bacterial isolate that was identified as *Flavobacterium* sp. NLM. F. sp. NLM was isolated during the Spring 2015 Microbiology course and will be the focus of future studies. (18)

Gehman, Courtney\*, Theresa Shafto, William Holl, and Erin Ventresca Albright College, Reading, PA 19604. Ingestion of diadzein leads to an increase in ERR-dependent larval lethality in Drosophila melanogaster. — Diet plays an important role in the cellular pathways responsible for metabolic regulation in living organisms. Previous studies in Drosophila melanogaster have shown that ingestion of soy products leads to a decrease in larval survival by preventing larval molting between instar stages. Because these molting stages are hormonally regulated, we hypothesized that this larval death may be due to isoflavones, plant-derived estrogen-like hormones, found in the soy products. When  $w^{_{118}}$  Drosophila were fed different concentrations of the isoflavone diadzein we saw that there was a significant increase in larval death when compared to the control. Based on its high homology to the estrogen receptor, we hypothesized that this increase in larval death is due to its interaction with the orphan receptor estrogen-related receptor (ERR). When Drosophila lacking the ERR were fed similar diadzein concentrations the previously reported larval death was abolished, supporting our hypothesis. This not only establishes diadzein as an ERR ligand, but may also be significant in possible dietary considerations in people suffering from triple negative breast cancer. This especially difficult to treat carcinoma is characterized by loss of typical therapeutic targets, such as the estrogen receptor and HER-2, however not only do patients express the ERR, but it is upregulated. A better understanding of the interaction of isoflavones with the ERR could open the door to more effective therapeutics. (73)

**Gehman, Keith\*, Andrew Farrell, and Derek Straub** Susquehanna University, Selinsgrove, PA 17870. *Biogas production as a function of feedstock in a lab-scale anaerobic digester.* — Anaerobic digestion of animal waste is a growing source of energy around the world. Food waste can provide a richer source of nutrients for microorganisms to break down, which can increase the gas yield of a digester. To study the effects of added food waste on the performance of an anaerobic digester, ten batch digesters were assembled and operated over several three week periods. Each 2 liter digester held 1.8 liters of swine manure effluent from an active digester. A feedstock of peeled, blended potato was added to three of the digesters. The same feedstock along with a sodium bicarbonate buffer was added to another three digesters. A third set of three digesters with no additions served as controls. One final digester containing only swine manure effluent was kept at room temperature while the other nine were kept at approximately 95°F in a warm water bath. Chemical oxygen demand (COD) was used as an indicator of the organic material available for digestion. The COD of each digester was measured before and after the three week digestion period. Based on the change in COD and measurements of gas production, an efficiency could be

calculated for each digester and used to compare digesters with added food waste feedstock and those without. (**171**)

Goldbach, Krysta\*, John Harms, and Lawrence Mylin Messiah College, Mechanicsburg, PA 17055. Characterization of T cell responses to a synthetic peptide representing a potential target for the immunotherapy of pancreatic cancer. - Pancreatic cancer is becoming more common and is one of the most lethal forms of cancer with a first-year survival rate of just 7%. Recent studies have discovered a correlation between a mis-spliced variant of the cholecystokinin (CCK) receptor expressed by pancreatic cells. While normal CCK receptors are responsible for binding of gastrin and signaling for enzymes to aid in digestion, this variant has been linked with increased cell proliferation, and autocrine stimulation that may enhance the outgrowth of aggressive pancreatic tumors. Because the variant form of the receptor only appears to be expressed by cancerous cells. the intron-encoded segment it retains represents a potential target for immunotherapy. In this study, we investigated whether immunization with a synthetic peptide corresponding to 20 amino acids located within the variant receptor intron-encoded sequence would stimulate the induction of T cells in C57Bl/6 mice. T cell responses were analyzed by using parallel ELISPOT and Intracellular Cytokine Staining (ICS) assays to: 1) measure frequencies of peptide-specific IFN-y-secreting cell numbers; and to 2) determine whether the responding T cells were of the CD4+ or CD8+ subset. The ELISPOT results confirmed a robust T cell response to the synthetic CCKCR peptide immunizations in two trials. Due to the low frequency of peptide-specific T cells, the ICS results were unclear, but may point to the induction of peptide-specific CD4+ T cells. Further efforts will utilize improved methods of immunization to generate higher frequencies of CR281-specific T cells. (113)

Goodson, Sara\*, and Deanne Garver Marywood University, Scranton, PA 18509. Characterization of Ellagitannins and Anthocyanins in Red Raspberry and Blueberry Leaf Extracts using LC/MS. -Flavonoids, such as ellagitannins and anthocyanins, have anti-inflammatory properties. Raspberry leaves have been reported to contain these flavonoids. In this study, raspberry leaves were extracted with ethanol and analyzed via liquid chromatography-mass spectrometry (LC/MS) techniques. The study was designed to confirm that the raspberry leaves contain these antiinflammatory agents and to compare the concentrations of these compounds in various sources of raspberry leaves. LC/MS techniques were also utilized with extracted blueberry leaves to determine if both leaves contain the same anti-inflammatory compounds. The concentrations of these flavonoids in raspberry and blueberry leaves were determined using LC/MS analysis. The concentrations will be compared to those found in brewed tea. Once the concentrations of flavonoids are known, more research will be done in order to determine what concentration of raspberry leaf tea would be needed to see the largest amount of anti-inflammatory effects. The goal of this study is to see if the flavonoids and anthocyanins in raspberry and blueberry leaves can be a natural alternative to pain medicines and help reduce joint pain and inflammation in patients with arthritis and tendonitis. (164)

**Grams, Nick\*, and Manuel Ospina-Giraldo** Lafayette College, Easton, PA 18042. *Role* of *Phytophthora sojae Pectate Lyase Enzymes in Glycine max infection.* — *Phytophthora sojae* is an oomycete that causes stem and root rot in the agriculturally relevant soybean species *Glycine Max*, and is responsible for over \$2 billion in losses annually. Developing resistance to *P. sojae* has proved to be a challenging task, as the pathogen has displayed a rapid evolutionary rate and is able to render many fungicides and soybean resistance genes inactive. Much remains unknown about the pathogen-host interactions that take place during *P. sojae* infection. It has been hypothesized that a critical component of the *P. sojae* pathogenicity process involves the early breakdown of plant cell walls by cell wall degrading enzymes (CWDE). Pectate is an essential structural polysaccharide in soybean cell walls, and the CWDE family of pectate lyases (PL) is responsible for eliminative cleavage of these polysaccharides leading to cell wall degradation. In an attempt to further understand the pathogen-host interactions that take place during *P. sojae* infection of *G.*  *max* the expression of *P. sojae* genes encoding PL enzymes was analyzed. Cultivars Williams and Williams 82, which are, respectively, susceptible and resistant to *P. sojae* infection, were inoculated with *P. sojae* mycelium. Plant tissue was collected at various points during infection and subjected to total RNA extraction. cDNA libraries were made using PL specific primers and were used in subsequent quantitative reverse transcription-PCR experiments to determine the transcriptional activity of PL genes. Results confirmed that *P. sojae* PL genes are actively expressed during infection; in addition, considerable differences in the level of up-regulation can be observed when the expression data from the interaction of *P. sojae* with the two cultivars are compared. These data suggest that PL genes may play an important role during early *P. sojae* pathogenesis. (**21**)

Gray, Jacob\*, Mohammed Ali\*, Mary Chey, and Narayanaswamy Bharathan Indiana University of Pennsylvania. Indiana, PA 15705. cDNA synthesis and cloning of tomato mosaic viral RNA (ToMV) using one-step nested RT-PCR. — Tomato Mosaic Virus (ToMV) a member of the genus Tobamovirus in the family Virgaviridae is composed of viruses with rigid rod virions that have a wide host-range infecting several crop plant species. It is a world-wide plant pathogen causing infection in more than 150 types of economically important crop species including vegetables and ornamental flowers. The virus is highly infectious and is very easily transmitted mechanically. The primary objective of this study is to recognize specific nucleic acid signatures that can be used to discriminate between determined strains of the same virus. We report results from spot nested-q-PCR-RFLP detection method of a strain of ToMV isolated from the field in Pennsylvania. Total RNAs were extracted from 0.1 g of leaves by using Ambion™ total Plant RNA Isolation Aid, and were used as templates for RT-PCR amplification with primers TobRTUP1 and TobRTD02. This method involves a one-step g-PCR using a combination of degenerate primers substituted of the coat protein gene that amplified part of the genomic region of the putative viral RNA. The cDNA thus generated was cloned into pJET suicide vectors. At least four independent clones were sequenced for each of the amplified fragments. The nucleotide sequences of these RT-PCR products were determined in both using Sanger sequencing with an ABI 3730 sequencer (Retrogen Inc. San Diego, CA). The sequences were compared for similarity against the non-abundant sequence databases of EMBL, EU, using the BLAST algorithm. The nucleotide sequences of the coat protein gene thus generated was compared with worldwide ToMV isolates and analyzed to assess the genetic structure and diversity of the Pennsylvania isolate. All the data analysis suggests that nucleotide diversity of the genus Tobamovirus within and between is different geographic regions was very low. The Data from such a strategy and cDNA clone analysis will be presented. (86)

Grill, Brooke\*, and Tammy Tobin Susquehanna University, Selinsgrove, PA 17870. Elevated soil temperatures from a Pennsylvania coal mine fire are associated with the increased presence of antibiotic resistance, antibiotic producing, and quorum sensing genes. - Centralia, a former mining location in Eastern Pennsylvania, is now known for its uncontrollable underground mine fire that began in 1962. Due to the resulting 56 year exposure to elevated soil temperatures, Centralia's bacterial communities provide unique insights into how bacterial competition and communication respond to environmental warming. Shotgun metagenomic analysis of soil samples from affected, recovered, and unaffected sites was completed and Cluster of Orthologous Gene (COG) data was used to identify genes involved in antibiotic resistance, antibiotic production and guorum sensing. These analyses showed that the prevalence of multi-drug transport, beta-lactamase, and transposase genes was significantly correlated to soil temperature. Penicillin-binding proteins and other antibiotic producing genes were also significantly correlated to soil temperature, as were some competence proteins related to quorum sensing. Covariance analysis further suggests that these three classes of genes are interrelated. These results suggest that bacterial competition and communication may increase during times of thermal stress, and may result in increased levels of horizontal gene transfer. (22)

Groves, Sarah Jane\*, Chelsea Mahoney, and Andre Walther Cedar Crest College, Allentown, PA 18104. Identification of Replication Protein A Phosphorylation dependent protein-protein interactions in Saccharomyces cerevisiae using the Yeast Two-Hybrid Assay. - In the United States the second leading cause of death is cancer, a disease that is caused mutations that lead to uncontrolled cell division. Genetic mutations arise during normal DNA replication and when errors occur in cellular DNA repair pathways. A main protein involved in DNA replication and repair pathways is Replication Protein A. RPA is a heterotrimeric, single-stranded DNA binding protein that can be phosphorylated on its second subunit and is known to interact with other proteins. While phosphorylated, protein-protein interactions with RPA may be altered. Our study focuses on identifying proteins that physically interact with Replication Protein A in a phosphorylation dependent manner in the model species Saccharomyces cerevisiae. In order to identify these proteins we utilized the Yeast Two-Hybrid assay. Yeast Two-Hybrid is a screening system that identifies protein interactions by measuring activation levels of transcription that occurs within physically interacting proteins. This assay was used to screen 6000 potential yeast protein candidates that interact with phosphorylated RPA. Of these 6000 strains, 300 potential candidates were identified and have been characterized to identify if they interact differently with phosphorylated versus unphosphorylated Replication Protein A. We have been working on isolating and sequencing the plasmids of selected RPA interacting candidates who show phosphorylation dependent interactions. These sequences are then identified by Basic Local Alignment Search Tool (BLAST) analysis. Having a better understanding of how Replication Protein A phosphorylation regulates interactions with other proteins will provide insights into RPA's role in cellular processes that often are dysfunctional within cancerous cells. (81)

Haase, Amanda\*, Deborah Austin, Kathryn Sarachan, and Brad Engle Wilson College, Chambersburg, PA 17201. Comparison of factors that affect the ethanol concentration in blood during putrefaction. - Determination of blood alcohol content (BAC) is important in some legal cases, and additional factors must be considered when determining BAC from a corpse. Ethyl alcohol concentrations detected post-mortem differ from those measured ante-mortem. Using an equine model, this study aimed to determine ethanol levels following a simulated state of putrefaction. Blood samples were collected, and then ethanol was added in vitro to simulate concentrations at the legal limit, half the legal limit, and twice the legal limit. To mimic normal putrefactive changes over the course of 24 hours, some samples were supplemented with one or both of the microbes, Escherichia coli and Candida albicans. In addition, trials were performed under anaerobic environments, blanketed with either nitrogen or carbon dioxide, to mimic gas conditions during the putrefaction stage of body decomposition. The final concentrations of ethanol under the varying microbial and gas conditions will be measured using gas chromatography-mass spectrometry (GC-MS) and compared with the amounts of ethanol initially present, the microbes present, and the gas conditions. The results from this study may aid in quantifying the effects of putrefaction on ethanol levels in post-mortem blood samples. (159)

**Haigh, Sydnie\*, and Anna Blice-Baum** Cabrini University, Radnor, PA 19087. *Tissue-restricted knockdown of the proteasomal component Prosalpha-3T may lead to reduced skeletal and cardiac muscle function in <u>Drosophila melanogaster</u>. — Heart and skeletal muscle cells need to maintain proteostasis for an organism to function properly. Proteostasis is important for all cells to maintain their function and thrive. Maintenance of proteostasis has been shown to be associated with decreased cell function. One pathway important to proteostasis is the ubiquitin proteasome system, which has been highly understudied in the context of cardiac aging. Prosalpha-3T is part of the proteasome, which is a cylindrical complex containing a core forming a central pore. The inner two rings within the pore comprise seven \beta subunits that contain three to seven protease active sites which are located on the interior surface of the rings, so the target ubiquitinated protein must enter the central pore before it is degraded. Through microarray analysis, we found that the* 

transcript of Prosalpha 3T was downregulated in control hearts with age, which may contribute to the negative phenotype associated with the aging heart. If the prosalpha-3T protein production is knocked down via RNAi in either heart or muscle cells specifically, protein could aggregate and cause an increase in ubiquitinated proteins within the cell. This can cause negative effects for cardiac and skeletal muscle function. A flight assay and lifespan analysis will be conducted in order to test whether the knockdown of gene expression affects the muscles controlling *Drosophila melanogaster* wings and heart. Heart function is especially important to study due to the extremely high percentage of deaths occurring in the U.S. that are directly related to heart diseases. We hypothesized that a decrease in flight ability as well as a shorter lifespan would be seen in the *D. melanogaster* that have Prosalpha-3T protein knockdown. (67)

Haile, Olivia\*, Allyson Owens, and Quven Aoh Gannon University, Erie, PA 16541. The Role of Ent Proteins in Nitrogen-Regulated Growth of <u>Saccharomyces cerevisiae</u>. — Cell membrane trafficking is the movement of important cellular cargo between the plasma membrane and organelles. In eukaryotic cells, trafficking plays a key role in proper nutrient uptake, which is essential to cell growth. We are examining the role of trafficking in regulating the localization of nitrogen permeases in the yeast Saccharomyces cerevisiae. More specifically how two clathrin adaptors, Ent3 and Ent5 regulate cell growth and affect trafficking of nitrogen permeases under preferred nitrogen sources ammonium and glutamine, and the non-preferred source proline. Ents are adaptor molecules that facilitate the trafficking of many proteins at the trans-Golgi network (TGN) and endosomes. We performed a growth curve assay in mutant cells with single or double deletion of Ent3 and Ent5 to examine cell fitness. Our preliminary data shows that deletion of Ent3 or Ent5 has no significant effect on growth in any of the nitrogen sources, but simultaneous deletion of both Ents causes a significant growth defect in the preferred nitrogen sources, suggesting that both Ent3 and Ent5 are required for robust growth in preferred nitrogen sources, but not in the non-preferred source. To assess the role of Ent3 and Ent5 on trafficking of nitrogen permeases, we monitored localization of the reporter permease Gap1 tagged with Green Fluorescent Protein (GFP) in ent3 $\Delta\Delta$  and ent5 $\Delta\Delta$ mutants in proline and ammonia, and no significant effect on Gap1 localization. The results from our study will give us a better understanding of the regulatory mechanisms that control nitrogen metabolism and cell survival. (99)

Hane, Kimberly\*, Julianna Marotta\*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. Optimization and analysis of the Nile Red efflux pump assay across bacteria species. -Multidrug resistance in bacteria is a major health concern, especially given the potential for derived cross-resistance between drugs, as exposure to one antimicrobial leads to derived resistance to other drugs neutralized through similar means. One general mechanism demonstrated to block the impact of multiple antibiotics is the enhanced activity of efflux pump genes, which remove a variety of compounds from the cell and prevent them from reaching their target. Our lab has demonstrated a potential link between triclosan-derived resistance in multiple bacteria species with enhanced efflux pump activity and would like to confirm this data via a Nile Red Assay, described by Bohnert et. al (2010) as a mechanism for measuring efflux pump efficiency in Escherichia coli cells. Cells are first energy-depleted through incubation in carbonyl cyanide *m*-chlorophenylhydrazone (CCCP), allowing for the accumulation of the lipophilic dye and consequential increased fluorescence. Reenergization of the cells with glucose activates the pump, decreasing fluorescence; the rate and extent of this decrease can be used to assess variations in efflux pump activity between bacteria strains. Species react differently to CCCP and protocol optimization must be conducted to determine the conditions for maximal energy-depletion. Incubation periods that are too short result in cells that do not accumulate Nile Red and thus have a low initial fluorescence; incubation periods that are too long result in cells that are unable to be re-energized. The study described here addresses the challenges faced in optimizing this protocol in cells that require short incubation periods (e.g. 10-60 minutes for Staphylococcus aureus), as compared to cells that require longer incubation periods (e.g. 8-20 hours for *E. coli* and *Enterobacter* species). This study provides a

starting point for use of this assay in a variety of species, and addresses its potential use in correlating role efflux pump function with triclosan resistance. (14)

Hannum, Courtney \*, Zachary High\*, and David Andrew Lycoming College, Williamsport, PA 17701. Genetic analysis of spontaneous grooming behavior in the fruit fly Drosophila melanogaster. - Repetitive behaviors are commonly associated with several human neurodevelopmental disorders. For example, restricted and repetitive patterns of behavior are a crucial diagnostic criterion for Autism Spectrum Disorder and are often concomitant with other neurodevelopmental disorders such as Fragile X Syndrome. The model organism Drosophila melanogaster can be used to study the genetic basis of such neurodevelopmental disorders, and specifically, how natural genetic variations influence behavior. This study examines the genetic variation in wild-type flies and its contributions to the phenotypic expression of grooming, an overtly spontaneous and repetitive behavior. Results show that there is quantitative variation in grooming behavior among various genetically distinct fly populations from the Drosophila Genetics Reference Panel. Through conducting a genome-wide association study, we have identified several candidate genes potentially associated with altered grooming. Previous research on these genes have demonstrated their implications in nervous system development, mechanosensory projection, and immune system regulation. Preliminary knockdown of the genes Mad, psh, and bun via RNA interference have shown significant influence on grooming behavior, providing sufficient reason to continue the functional validation of these candidate genes. (76)

Hanumaihgari, Priyanka\*, and André Walther Cedar Crest College, Allentown, PA 18104. Examining genotoxicity of consumer products using a novel eukarvotic differential assay. --According to the CDC, there may be a correlation between toxicity in consumer products and increased health risks. Due to current limitations on standard toxicity tests, specifically the industrystandard Ames test, there is a necessity for improved testing. The goal of this project is to create an effective method to examine the toxic and genotoxoic potential of various consumer products, and to analyze the type of DNA damage being caused by consumer products. This novel assay will use the eukaryote Saccharomyces cerevisiae, strains Wild Type, ku70, rad10, rad52, and meC1, to examine the genotoxicity of common consumer products by using mutated repair pathways. Initially, a Kirby-Bauer test will be used to analyze the toxigenic potential of various hairsprays and will involve testing high doses of chemicals on yeast-covered plates. To examine genotoxicity, yeast will be grown on different doses of the toxic chemical to establish a dose-response relationship. Data collection includes measuring the diameter of the zone of inhibition in the Kirby-Bauer test and counting the number of yeast cells in the genotoxicity assay. Different sensitivities of each yeast strain to the hairsprays should indicate if DNA damage is being caused by the products. In addition, a Chi-square test will be used to determine which chemicals in the products are responsible for DNA damage. The results show that 5 of the 22 tested consumer products displayed toxicity, and 4 caused a greater effect on the ku70 mutated yeast strain, suggesting genotoxicity. Overall, this new assay will be more sensitive than existing toxicity tests and suggest a more effective way of testing product hazard. (25)

**Harris, Sebastian\*, and Thomas LaDuke** East Stroudsburg University, East Stroudsburg, PA 18301. *Microhabitat selection by gestating timber rattlesnakes (<u>Crotalus horridus</u>) in northeastern <i>Pennsylvania.* — Timber Rattlesnakes (*Crotalus horridus*) are becoming increasingly rare in the Northeastern portion of their range. Studies on habitat selection in areas where they continue to thrive is essential for future recovery plans. Reproductive females are particularly vital components to healthy populations, and understanding habitat essential to them is important for their preservation. We sought to discern whether gravid females selected habitat with particular microhabitat features on a fine scale. A total of twelve habitat variables were compared between occupied (N=19) and unoccupied rocks within an expansive tract of state game land in Northeastern Pennsylvania. Results of our binary logistic regression found distance to nearest overstory tree to be a significant predictor variable. Gestation rocks were further on average from

overstory trees than unoccupied rocks. This aligns with our understanding that gestating Timber Rattlesnakes prefer open habitat with ample sun exposure. In addition, rock volume estimates for occupied rocks were found to be significantly greater than rocks at unoccupied subsites. Results from our Principal Component Analysis indicate gestating females in our study utilize larger rocks with a variety of shapes. Larger rocks could provide a greater variety of thermal opportunities and/or facilitate congregations of gravid females and neonates. Aside from distance to nearest overstory tree and rock volume, habitat variables assessed in our study were not found to be significant features of gestation habitat for Timber Rattlesnakes. Supplemental research could reveal critical components of gestation habitat for *Crotalus horridus*. (124)

**Hearne, William\*, and Isaac VonRue** Kings College, Wilkes-Barre, PA 18711. *Modeling the Multiple Melting Peaks of Poly(ɛ-caprolactone) Thermoreversible gels.* — It has been observed that poly(ɛ-caprolactone), PCL, homopolymer thermoreversible gels exhibit an interesting phenomenon of having multiple melting peaks. The research project has focused on how solvents, dimethylformamide and acetonitrile, and conditions, such as annealing temperature and PCL concentration, contributed to the observed melting ranges of the gels using differential scanning calorimetry, DSC. It was found that up to four melting peaks could be observed for PCL-acetonitrile gels at very specific sets of PCL mass fractions and annealing temperatures. It is theorized that the multiple melting peaks are due to gel lamellae that are of varying degrees of order. The more disordered lamellae are thought to melt first and then recrystallize on the lamellae of higher order. The data obtained from the DSC experiments gives a signal where the endothermic peaks from melting the gel and the subsequent exothermic recrystallization peaks are combined. It is hoped that by using fast Fourier transformations, each individual endothermic and exothermic peak can be isolated. Using these isolated signals, it will be possible to construct a model to show how annealing temperatures affect the populations of lamellae. (**172**)

**Heil, Elysia\*, and Nicholas Sizemore\*** University of Scranton, Scranton, PA 18510. *Computational analysis of intermolecular Diels–Alder reactions of α-amido acrylates with N-Cbz-1,2dihydropyridine and cyclopentadiene.* — Recently, a synthetic method for the intermolecular Diels– Alder reaction between α-amido acrylate dienophiles with cyclic dienes was developed by Spivey et al. The products of these cyclization reactions were mixtures of endo/exo stereoisomers. In order to understand the factors governing stereoselectivity and increase the reaction's utility, a computational study was undertaken in an effort to identify a computational method of analysis that is consistent with the synthetic experiments. Conformational analysis (MMFF) was carried out for the starting materials, transition state estimates and products using the Spartan molecular modeling program (Spartan'16). Low energy conformations for each molecule were then evaluated using density functional theory calculations at the B3LYP 6-31G(d) level of theory using Gaussian09. The results of this computational study will be described herein. The calculated energy values will be compared to experimental results of Spivey et al. to determine if computational analysis of reactions supports the stereoselectivity seen in physical experimentation. (4)

**Helms, Anne, and John Campbell\*** Mercyhurst University, Erie, PA 16546. *Exploring the possibility of transplanting net spinning caddisflies (Trichoptera) to a recently restored urban stream in Erie PA.* — Cascade Creek in Erie PA has been the subject of extensive restoration efforts over the past ten years with the final stage completed in 2014. While a great deal of attention was focused on bank stabilization and restoration of the riparian zone, little attention was directed toward active repopulation of the aquatic insect community. Habitat improvement and efforts to improve water quality have not appeared to result in the return of pollution-sensitive aquatic invertebrates, since stream inventories conducted as recently as January 2018 have shown that macroinvertebrate diversity has remained poor. with nearly minimal biotic diversity. The purpose of this study is to demonstrate feasibility of transplanting caddisfly larvae from one stream to another as a means of mechanically augmenting the aquatic insect community. The underlying assumption is that stream

restoration is a multistep process and success might be possibly achieved by directly reintroducing lost faunal elements. (**134**)

Hill, Brianna\*, and Andre Walther Cedar Crest College, Allentown, PA 18104. Examining the role of phosphorylation on RPA genetic interactions with DNA repair genes KU70 and RAD52. -According to the American Cancer Society, in 2018 there will be 1,735,350 new cancer cases diagnosed and 609,640 people are expected to die from cancer-related causes in the United States alone. Current chemotherapeutic cancer treatments are non-specific and target actively dividing cells. This leads to damage in the patient's healthy cells, leading to unwanted side effects and decreasing the efficiency of the treatment. An increase in specificity of chemotherapeutic drugs would greatly reduce the death of healthy cells by treatment. In order to understand how to best target specific mutations in cancer cells, the role of the highly-conserved, single-stranded DNA binding protein, Replication Protein A (RPA), needs to be better understood in DNA replication, DNA repair, cell cycle control, and telomere synthesis. Previous research has shown that RPA becomes phosphorylated in response to DNA damage, but the exact role of phosphorylation in the cellular response to damage is still unknown. The objective of this research is to ascertain the effect of RPA phosphorylation on the cellular response to DNA damage by identifying genes involved in DNA repair mechanisms that genetically interact with RPA. Specifically, in this research, the potential genetic interactions between RPA and the repair genes KU70 and RAD52 will be observed. Rad52p is involved in homologous recombination, and Ku70p is involved in nonhomologous end-joining. A clearer picture of RPA's role in DNA repair and its interactions with other genes will allow for a better understanding of the underlying causes of cancer and more specific chemotherapeutic drugs. (105)

Howell, Gregory\*, and Bridgette Hagerty York College of Pennsylvania, York, PA 17405. Redbacked salamanders (Plethodon cinereus) as indicators for recovery of habitats along closed roads in Spring Valley County Park, York, PA. - Roads make up a small percentage of the total land area in the United States, but they ecologically affect a much larger portion of the land area because of the impacts they have on the surrounding landscape. Roads change the physical characteristics of an ecosystem, which is important for salamanders that require very specific environmental conditions. Spring Valley County Park, located in South Central Pennsylvania, closed several roads to public use in 2013. We hypothesized that if salamander abundance has increased near these closed roads compared to open roads that edge effects have decreased and improved habitat for terrestrial salamanders. Quadrats centered on perpendicular transects at distances of 0, 5, 10, 20, 40, and 80 meters were surveyed in areas with closed and open roads. We measured abundance of terrestrial salamanders, soil moisture, air and soil temperature, soil pH, leaf litter depth, light intensity, the number of cover objects, and cover object area at each quadrat. Abundance of *Plethodon cinereus* along perpendicular transects was similar between closed and active roads. Furthermore, all environmental factors were similar between closed and active roads. However, soil pH was significantly more basic at distances closer to closed and active roads. The ecosystem in Spring Valley Park may require more time to respond to the changes in the environment that come with closing a road. Removing roads can be very costly and time consuming, however, if ecosystem recovery can happen without road removal, this is a relatively simple way to improve habitats without having to spend money and resources. (31)

**Huggins, Charity\*, Kyle Retterstoff, and Daniel Curlik II** York College of Pennsylvania, York, PA 17405. *Operant conditioning increases the number of surviving cells in the ventral dentate gyrus of the adult rat.* — Thousands of new neurons are produced each day in the dentate gyrus of the adult hippocampus. However, the majority of these cells will die within weeks of their birth. The most effective way to prevent the death of these cells is through effortful and successful learning. Myriad studies have revealed that classical conditioning and spatial learning can prevent this cell death. However, little research has examined whether acquisition of an operant conditioning task also increases the number of surviving neurons. Therefore, the current study was conducted to

determine whether training with an operant procedure would prevent the death of adult-born hippocampal cells. Adult male rats were trained with fifty trials of an operant discrimination procedure per day, for four consecutive days (N=14). In order to motivate animals to perform this task they were food restricted prior to training. Additional animals were food restricted, but not trained (N=7). Another group of animals were not food restricted, and not trained (N=5). Surprisingly, food restriction significantly decreased the number of surviving cells in the granule cell layer of the dentate gyrus. Food restricted untrained animals retained fewer cells than non-food restricted untrained animals (p < 0.05). However, training with an operant task prevented this decrease. This effect was largely driven by the ventral region of the dentate gyrus. Trained animals retained more new cells than food restricted untrained animals in the ventral granule cell layer (p < 0.05) and the overall ventral dentate gyrus (p < 0.05). Together, these results indicate that food restriction decreased the number of surviving cells, however operant conditioning attenuated that decrease. As task difficulty has been shown to modulate the effect of learning on cell survival, future experiments will determine whether more difficult to acquire operant procedures also prevent the death of these cells. (**56**)

**Inserra, Kasie\*, Priscilla Thomas, and Quyen Aoh** Gannon University, Erie, PA 16541. *Role of SCAMP3 in CXCR4 Trafficking*. — The CXC-Chemokine Receptor Type 4, CXCR4 is a G-protein coupled receptor involved in the metastasis of cancerous tissue. Dysfunctions in trafficking of CXCR4 may contribute to its overexpression in cancer. In this study, we are examining the role of the Secretory Carrier Membrane Protein, SCAMP3 in regulating CXCR4 trafficking. SCAMP3 interacts with proteins that also regulate CXCR4 trafficking, including the ESCRT proteins Hrs and the ubiquitin ligase ITCH. Using RNA interference and a well characterized immunofluorescence, we are examining CXCR4 trafficking in the presence and absence of SCAMP3. We predict that SCAMP3 could promote or inhibit degradation of CXCR4. If correct, then our studies will reveal that SCAMP3 is a novel regulator of CXCR expression. In our preliminary experiments, we our optimizing our immunofluorescence conditions to detect internalized CXCR4. We have found that briefly permeabilizing the cells before fixation improves detection of CXCR4. Next, we will determine if knockdown of SCAMP3 affects CXCR4 trafficking to the lysosome. (100)

Isaga, Emily\*, Arielle Raugh, and Lawrence Mylin Messiah College, Mechanicsburg, PA 17055. Does a robust CD8+ killer T cell response alter the type(s) of cytokines secreted by CD4+ helper T cells responding to the same tumor antigen? - The relationship between killer CD8+ T and helper CD4+ T cells is important in understanding how cell mediated immunity can be trained to combat cancer by appropriate vaccination. The Simian Virus 40 Large T antigen (SV40 T ag) oncoprotein contains multiple CD8+ and CD4+ T cell epitopes of varying immunological potencies. The goal of this study was to determine if a robust CD8+ T cell response influenced whether the cytokines IL-10 and/or IFN-g would be secreted by CD4+ T cells induced by epitopes within the same antigen. Mice were immunized with cells expressing the wild type SV40 T ag (B6/K-0 cells) to generate a robust CD8+ T cell response, or with cells expressing a mutated SV40 T ag (B6/K-1,4,5 cells) lacking immunodominant CD8+ epitopes. Both T antigens contained three CD4+ T cell epitopes (381, 529, 581) against which T cell responses were monitored. MHC class I tetramer staining and flow cytometry were used to measure the magnitude of the CD8+ T cell response induced by each immunization. Flow cytometry confirmed that B6/K-0 immunizations induced a robust CD8+ T cell response while B6/K-1,4,5 immunizations did not. Single color, parallel ELISPOT assays were used to measure the frequencies of IFN-g- vs. IL-10-expressing T cells specifically recognizing each of the three CD4+ epitopes. Results from the parallel single color ELISPOT assays indicated that IFN-g-secreting T cells were far more frequent than IL-10-secreting T cells following immunization with B6/K-0 cells. The frequency of IL-10- secreting T cells did not exceed the frequency of IFN-g-secreting T cells following immunization with either cell line. These results failed to support our previous hypothesis wherein the ratio of IL-10 vs. IFN-g secreting T cells would be

strongly influenced by the presence of CD8+ T cells responding to epitopes within the same antigen. (**114**)

**Jacobs, Kyle\*, Jessica Hoffman\*, and Jeffrey Newman\*** Lycoming College, Williamsport, PA 17701. *Reinstatement of the genus <u>Epilithonimonas</u> within <u>Flavobacteriaceae</u> and isolation of <u>Epilithonimonas diehlii sp. nov.</u>, from a freshwater creek. — As part of an undergraduate Microbiology course, a novel orange pigmented, Gram-staining negative, rod-shaped, non-motile bacterial strain belonging to <i>Flavobacteriaceae* was isolated from a freshwater creek. Its identification led to comparative phenotypic and genomic studies with closely related reference strains that had recently undergone reclassification. The genus *Epilithonimonas* was established with the description of *E. tenax*, but has since been moved into the genus *Chryseobacterium* along with several other species that cluster with this organism. Here we argue that this cluster forms a monophyletic group based on characteristics that distinguish it from

"true" *Chryseobacterium* species such as Average Amino Acid Identity (AAI), fatty acid composition, G+C content and large genome size. We propose that the genus *Epilithonimonas* be reinstated with *E. tenax* as the type species; and that the former members, as well as

seven *Chryseobacterium* species be moved into the genus *Epilithonimonas*, including *E. lactis*, *E. xixisoli*, *C. zeae*, *C. hungaricum*, *C. hominis*, *C. caeni*, *C. molle*, *C. pallidum*, and *C. bovis*. The sequence of the 16S rRNA gene of the novel strain, designated FH1<sup>T</sup>, was 98.1 – 96.9% similar to those of *Epilithonimonas lactis*, *Epilithonimonas xixisoli*, and *Epilithonimonas tenax*. Comparison of whole genome shotgun sequences demonstrated genomic uniqueness with average nucleotide identity (ANI) values below 86.3%. Polyphasic characterization and comparison to these relatives revealed that strain FH1<sup>T</sup> was similar to other *Epilithonimonas* strains in that it contained MK-6 as its major respiratory quinone; produced flexirubin-type pigments, oxidase and catalase; and primarily contained the fatty acids iso-C<sub>15:0</sub>, anteiso-C<sub>15:0</sub>, and summed feature 3 comprising iso-C<sub>15:0</sub>2-OH and/or C<sub>16:1</sub> $\omega$ 7c. The DNA G+C content is 36.9 mol%. Based on the results of this study, strain FH1<sup>T</sup> represents a novel species for which the name *Epilithonimonas diehlii* sp. nov. is proposed. (**19**)

Jacobson, Bradley, Kevin Cooney, Devin Kelly, Drake Burgess\*, Michael Cendoma, and Dustin Bruening Mercyhurst University, Erie, PA 16546. Cervical spine movement during American football equipment removal: supine versus torso tilt, spine board versus turf. - Background: In 2001, the NATA released the Inter-Association Pre-Hospital Care of the Spine Injured Athlete position statement describing that the equipment of a football athlete with a suspected cervical spine injury is to remain on, or if any equipment needs to come off, all equipment is to be taken off prior to transport to a medical facility ("All or Nothing Endeavor"). In 2015, the NATA and the Inter-Association Task Force released a consensus statement recommending removal of an athlete's equipment prior to transport. Purpose: To determine which on-field equipment removal procedure created less cervical spine motion and is safer for the injured athlete. Hypotheses: The torso tilt equipment removal procedure would create greater movement of the cervical spine in relationship to the torso when compared to supine equipment removal procedures; Removal of football equipment on the turf surface would create greater movement of the cervical spine in relationship to the torso as compared to a spine board. Methods: A trackSTAR electromagnetic motion capture system measured the angular movement and the linear displacement between the skull and the manubrium during the supine and torso tilt equipment removal techniques from subjects in different weight categories. Data Analysis: Data was analyzed in custom written Matlab software with a 2x2x3 ANOVA and significance of 0.05. **Results:** Linear displacement (spine board): 7.88 ± 1.92 cm. supine; 10.69  $\pm$  3.52 cm. torso tilt. Linear displacement (turf): 8.01  $\pm$  2.09 cm. supine; 11.02  $\pm$ 2.91 cm. torso tilt. Angular displacement (spine board):  $16.32 \pm 5.85$  supine;  $18.63 \pm 6.64$  torso tilt. Angular displacement (turf):  $16.69 \pm 6.65$  supine;  $19.60 \pm 8.48$  torso tilt. **Conclusions:** The surface had no significance on cervical spine motion. The torso-tilt technique measured to have

significantly more linear displacement and angular displacement than the supine technique, making the latter safer. (59)

**Jain, Avijita, Ty Stewart\*, and Denali Davis\*** Indiana University of Pennsylvania, Indiana, PA 15705. *Inhibition of DNA amplification by photoactive Ru(II) and Ru(II)Pt(II) based polypyridyl complexes using PCR studies.* — Sterically strained Ruthenium based metal complexes represent an emerging class of bioactive molecules capable of undergoing photoinduced ligand exchange. These complexes exhibit covalent interaction with DNA upon light irradiation. Using polymerase chain reaction, we examined the extent of inhibition of DNA replication by the previously reported Ru(II) complex, [Ru(biq)<sub>2</sub>dpp](PF<sub>6</sub>)<sub>2</sub> and Ru(II)Pt(II) bimetallic complex, [Ru(biq)<sub>2</sub>dppPtCl2](PF<sub>6</sub>)<sub>2</sub> (biq = 2,2'-biquinoline, dpp = 2,3-bis(2-pyridyI)pyrazine) in dark and upon photoirradiation. These results were compared to the well-known anticancer drug, cisplatin, with respect to concentration and effects on replication. Reported results will demonstrate that the designed complexes exhibit enhanced inhibition of DNA amplification upon photoirradiation thus making them promising photodynamic therapy agents. (**166**)

Jandu, Narveen, and Cheyenne Annarumo\* Gannon University, Erie, PA 16541. Influenza-like illness and vaccination rates amongst college students based on housing style. -Background: A college campus provides a unique setting for the ease of transmission of various infectious disease agents. Housing styles can vary from off-campus to on-campus, with room-mates or without room-mates, shared bathroom facilities or private facilities. Regardless of housing style, students will share many other common spaces (i.e. study spaces, dining areas and social rooms). The aim of this study was to determine if campus housing style impacts the frequency of influenza-like illness amongst college students. Methods: In this study, an online survey was used to determine the influenza vaccination status, housing-style and frequency of illness amongst college students. Survey responses were collected from Oct. 1, 2017 to Jan. 1, 2018. A total of 290-students consented to completing the online survey. **Results**: The majority of respondents, 63% (n=183) indicated that they received the influenza vaccine, while the remaining 37% (n=107) did not receive the influenza vaccine. In relation to housing-style, the majority of freshmen (56%) live in on-campus suite-style residence with private bathrooms, the majority of sophomores (67%) live in on-campus apartments with private bathrooms, some juniors (31%) may still be living in these on-campus apartments, while some juniors (38%) have transitioned to off-campus housing; and most seniors (61%) are living off-campus. Regardless of housing, 55% of respondents self-reporting getting sick a few (3-5) times per year. In comparison, to their previous year on campus, however, 49% of respondents indicated that they were less sick in subsequent years compared to previous years. Conclusion: College students are susceptible to influenza-like illness in-part due to close proximity in living arrangements and sharing. As students transition through their years of college, changes in their living arrangement (from on-campus to off-campus) and other lifestyle choices will result in less cases of illness throughout the year. (10)

**Jandu, Narveen, and Matthew Dilts**\* Gannon University, Erie, PA 16541. *Antibiotic resistance in <u>Enterobacter aerogenes</u>. — Background: Antibiotic resistance is a growing problem around the world, with no sign of stopping. Drug resistance is especially concerning and alarming in the healthcare setting, where seemingly innocuous microorganisms have the capacity to become problematic and even deadly. For instance, <i>Staphylococcus epidermidis* is a Gram-positive microorganism that is part of the human microbiome and a normal inhabit of the skin. But this microbe can cause infections in the hospital setting including urinary tract infections, infections at indwelling medical devices and even septicemia. *Enterobaccter aerogenes* is a Gram-negative rod-shaped organism that is a normal inhabitant of the gastrointestinal tract of warm-blood animals. *E. aerogenes* is responsible for numerous infections, sch as respiratory tract infections, urinary tract infections, urinary tract infections, and bacteremia. The CDC ranks Enterobacter species as one of the most common sources of nosocomial infections from the Enterobacteriaceae family. In 2017 *E. aerogenes* was

identified by WHO as a top priority for global research and drug development. The **objective** of this study is to compare the viability and growth response of *S. epidermidis* and *E. aerogenes* to multiple antibiotics. **Methods**: The Kirby-Bauer antibiotic susceptibility disk diffusion assay and the minimum inhibitory concentration assay were used as complementary assays of antibiotic susceptibility. **Results**: Using the Kirby-Bauer assay, antibiotic susceptibility to six-antibiotics were evaluated. *S. epidermidis* and *E. aerogenes* showed similar zones of inhibition (ZOI) to ciprofloxacin (5ug/mL), streptomycin (10ug/mL), trimethoprim (5ug/mL) and chloramphenicol (30ug/mL). In response to penicillin (10ug/mL), *E. aerogenes* generated the smallest zones of inhibition (ZOI) of <6 mm, while *S. epidermidis* generated a larger zone of inhibition (ZOI) of >16mm. In response to tetracycline, *E. aerogenes* generated a zone of inhibition (ZOI) of ~14 mm, while *S. epidermidis* generated a zone of inhibition (ZOI) <6 mm. (**11**)

Jones, Claire\*, Christine Rittenhouse, and Ann Yezerski Kings College, Wilkes-Barre, PA 18711. Single Nucleotide Polymorphisms (SNP's) associated with dyslexia may influence college major choice in the King's College community. – Developmental dyslexia is a heritable neurodevelopment learning disorder that causes reading difficulties despite intelligence. Dyslexia is often diagnosed in the early childhood years, but continues on with the child throughout their lifetime, which may influence their educational and career pathways. Through linkage studies, there have been at least nine different susceptibility loci identified that may influence dyslexia. The ongoing study has examined the candidate genes of FMR1, KIAA0319, EKN1, and ROBO1, by genotyping ten different single nucleotide polymorphisms (SNPs) in these genes along with the 5' UTR CGG region on the X chromosome. The FMR1 gene, known for being involved in Fragile X Syndrome, is the only candidate gene that is on the X chromosome. Also, its association with mental retardation goes against the definition of dyslexia. Our current research project is to collect genotyping data for FMR1 to add to our previous data sets for the other loci. Our previous results, using DNA extracted from 200-300 King's College students and faculty, have indicated a connection between major choice and SNPs in the KIAA0319 and ROBO1 loci with science majors having higher dyslexia-associated genotypic frequencies. Preliminary results using our newly designed genotyping methods for the FMRI gene has also shown promising results that follow the previous pattern, but low sample size in the pilot study prevented any statistical significance. (82)

Jones, Rebekah\*, and John Harms Messiah College, Mechanicsburg, PA 17055. Optimization of RNA Isolation from Frozen Human Pancreatic Cancer Tissue. — Pancreatic cancer has a dismally low five-year survival rate of 4%. Our lab has focused on the etiology of CCK2<sub>14sv</sub>R, a hyperactive splice variant of the gastrin receptor (CCK2R), which has been associated with increased pancreatic tumor aggressiveness. To determine if a correlation exists between a single nucleotide polymorphism (SNP) in the receptor, and expression of the variant RNA in patients, we aim to genotype human pancreatic tumor samples and quantify CCK2R and CCK2<sub>iss</sub>R mRNA. Due to the highly fibrotic nature of pancreatic cancer and the friable nature of RNA, we undertook the following study to optimize the isolation of RNA and qDNA. Tissue (7-19 mg) was ground via mortar and pestle and processed via RNeasy Mini kit (Qiagen) paired with QIAshredder for homogenization. Yields were typically low (<0.2 µg/mg tissue). Employing needle homogenization in place of the QIAshredder resulted in a 2-fold increase in RNA (0.5 µg/mg tissue), while using guanidinium thiocyanate-phenol-chloroform extraction prior to the kit lysis buffer also led to a 2-fold increase (0.5 µg/mg tissue). Neither of these modifications, alone, provided the necessary RNA yield for later analyses; however, preliminary data suggest that, in combination, an 18-fold increase in yield (4.4 µg/mg tissue) is achievable. Additionally, this modification permits parallel isolation of gDNA from the same tissue sample, while retaining the purity and efficiency advantages of the spin column isolation. (110)

**Joyce, Erin \*, and Anna Blice-Baum** Cabrini University, Radnor, PA 19087. *UBC84D knockdown may lead to decreased cardiac and skeletal muscle performance in <u>Drosophila melanogaster</u>. — Proper cardiac and skeletal muscle performance is dependent upon maintaining appropriate gene* 

expression. Dysregulation of the expression of particular genes can alter myocyte function and structure. Heart cells need to maintain adequate proteostasis in order for the whole heart to contract properly, especially since these cells are unable to replicate once they have differentiated. Additionally, aging of *Drosophila melanogaster* is associated with weaker cardiac muscle and thus functional decline. UBC84D is an E2 ubiquitin conjugating enzyme that plays a role in accepting activated ubiquitin from E1 enzymes. This transfer then activates ubiquitin ligases to ubiquitinate target proteins. Transcripts of this gene were shown previously to be differentially expressed in a microarray analysis of FOXO-overexpressing hearts versus control hearts over time. However, the study of ubiquitin-conjugating enzymes, specifically in cardiac aging, has been a highly understudied area If UBC84F is knocked down in *D. melanogaster* using conditional RNAi, it is hypothesized that the cardiac and skeletal muscle function will decline acutely. We will test this hypothesis by performing flight assays on flies modified such that only indirect flight muscle has UBC84D knockdown (MHC-Gal4 and Mef2-GAL4 drivers) and lifespan analyses on flies with UBC84D RNAi knockdown only in the heart at different doses (GMH5-GAL4 and TinCD4-GAL drivers). **(68)** 

Kalesnik, Arek\*, and Emily Basile Cabrini University, Radnor, PA 19087. Measuring aquatic ecosystem health using acetylcholine esterase (AChE) activity in freshwater amphipods. -Acetylcholine Esterase (AChE) breaks down Acetylcholine (ACh), a neurotransmitter primarily concerned with directing nerve impulses to induce motor function in organisms. Certain stressors can inhibit enzyme activity, causing the over accumulation of both ACh and AChE, with the former leading to paralysis and starvation; many insecticides cause this inhibition. Insecticide use can lead to chemical runoff, contaminating local aquatic ecosystems, causing a cumulated or direct impact on local populations. Observing AChE activity in organisms can reflect the health of an ecosystem, indicating pollution, infections, diseases, and other stressors, and is therefore a biomarker assay performed by ecologists. For this experiment, AChE activity was measured in a model organism, an aquatic amphipod from the family Gammaridea. Samples were collected from leaves using both the leaf pack technique, as well as hand collection. The samples were taken from two sites with varying levels of human disturbance along Crabby Creek, in Eastern Pennsylvania: Crabby Creek Park (CCP) was the less impacted by human disturbance compared to West Lakes Drive (WLD). For that reason, it was expected that CCP would show higher amounts of AChE activity, indicating low potential for water contamination. The results showed no statistical difference between the two sites, while there did appear to be a trend towards lower enzyme activity in WLD samples. This lack of significance could be due to a relatively small sample size. Further testing with larger amounts sample per site would be required to determine if there was any real difference between the two ecosystems. If there were an indication of statistical significance, further testing would be necessary to determine the cause of variation, such as toxicology screenings, genetic mutations, etc. (**130**)

**Kalimon, Olivia\*, Widzowski, Daniel** Indiana University of Pennsylvania, Indiana, PA 15705. *Validation of a neurobehavioral assay for testing 5-HT2A activity of novel compounds: dose-effect characterization of mirtazapine.* — Mirtazapine is an atypical antidepressant that blocks various neuroreceptors and has also been shown to reduce methamphetamine dependence; however, there are also negative side effects due to the drug's lack of binding specificity. We want to discover a drug similar to mirtazapine that will block serotonin 5-HT<sub>2</sub> receptors, specifically in receptor 5-HT<sub>2A</sub>, that will maintain the positive effects and lose the undesirable ones. We demonstrated that selective 5-HT<sub>2A</sub> antagonist volinanserin, and inverse agonist pimavanserin both dose-dependently reduce 5-HTP-induced head twitch in mice. Ongoing studies are testing mirtazapine and related compounds. Results from these studies will aid in the interpretation of studies of mirtazapine-induced weight gain or loss. Determining dose-response curves for this mirtazapine and other compounds used in humans will provide a basis for mechanistic studies and translating doses from mice to humans. (**58**)

Khoj, Maisa\*, Seema Bharathan, and Narayanaswamy Bharathan Indiana University of Pennsylvania, Indiana, PA 15705. Analysis of cloned viral Double-Stranded (ds) RNA from selected isolates of Rhizoctonia solani belonging to Anastomosis Group (AG)-4. - Rhizoctonia solani is a soil-borne fungus that is considered to be an economically important pathogen of crop plants. It is classified into different anastomosis groups (AG's) based on their hyphal interactions, host specificity, pathogenicity and colony morphology. My research focuses on the two isolates Rhs113 and Rhs114 that are hetrokaryons and belong to AG-4. Mycoviruses that infect fungi have doublestranded (ds) RNA genomes. These dsRNA are cytoplasmic and viral in origin. The main objective of this project is to compare dsRNA sequences between cloned dsRNA from the isolates Rhs113 and Rhs114. Serotype variations are common among viruses suggesting that biotype variations could also occur. In the lab, the dsRNA of Rhs113 isolate was purified. The following sizes of dsRNA were obtained; one band was larger than 5 kb and the other was 3 kb. DsRNA's were reverse transcribed into cDNA and ligated into p-jet cloning vector (Fermentas). Ten plasmids of Rhs113 and 3 of Rhs114 were purified then fast digested using EcoRI enzyme. DsRNA and plasmids products were analyzed by gel electrophoresis. The largest 7 kb fragment containing the presumptive full length cDNA clone of Rhs114 was further selected for sequencing and primerprobe design. The cloned fragment was sequenced by Sanger sequencing with an ABI 3730xL sequencer (Retrogen, Inc. USA). Following sequencing, the forward primer (GCTGGTCCTCCTCATACTTGA), reverse primer (CGCAGGCCGTCTTTGAGATAC) and the probe (5'Fam-CTCCACGGGAAGAAACATGCGGCT-BHQ1) were designed using BLAST sequence via Biosearch Technology. The conventional and Real-Time PCR analysis will be done using Bio-Rad g Cycler and Eppendorf RealPlexc© Real Time PCR Thermocycler, respectively. The results from both techniques will be presented which will include Ct values, amplification, and specificity of nucleic acid hybridization. Preliminary results indicate a Ct value of 6 from plasmid DNA of Rhs114 and Rhs 113 suggesting considerable sequence homology between dsRNA from Rhs113 and

Rhs114. (**87**)

**King, Carli\*, Emily Carson, and Jeffrey Newman** Lycoming College, Williamsport, PA 17701. <u>Sphingobacteriaceae</u> related to <u>Pedobacter agri</u> isolated from a freshwater creek. — As part of an undergraduate microbiology course, a pink-pigmented, Gram-staining negative, rod-shaped bacterial strain designated BMA was isolated from a creek in north-central Pennsylvania during winter of 2014. Comparative 16s rRNA sequences identified the closest match to several *Pedobacter* species. Full genome sequencing of the isolate and reference type strain revealed an approximately 80% average amino acid identity relative to other pink-pigmented species *Pedobacter agri, Pedobacter borealis,* and *Pedobacter alluvionis,* which falls below the threshold of 95% for different species. When compared to the yellow-pigmented type species *Pedobacter heparinus,* an average amino acid identity below 70% was found, which suggests that these organisms should be in separate genera. Based on genotypic and phenotypic analyses, strain BMA represents a novel species within the family *Sphingobacteriaceae*. Many species within the genus *Pedobacter* are highly divergent from the type species suggesting that significant reclassification into new genera is required. (**20**)

**Kornblum, Emily \*, and Christine Proctor** Harrisburg University of Science and Technology , Harrisburg, PA 17101. *Coral bleaching in response to higher average regional ocean surface temperatures.* — With rising global ocean temperatures, the frequency of coral bleaching events is predicted to increase, becoming an annual reef event. Coral are important ecosystems providing tourism, fishing, shoreline protection, and increased biodiversity. Although coral bleaching does occur naturally, anthropogenic induced climate change is believed to decrease the amount of time between bleaching events, making it more difficult for coral to recover. Some studies suggest that coral in the Pacific and Indian oceans are adapting to increasing ocean temperatures while coral in the Caribbean are not showing signs of adaptation. However, most coral studies focus on small localized data sets. Using a global coral bleaching database containing over 7,000 recorded bleaching events (Donner, Rickbeil, and Heron, 2017), this study investigated the relationship between bleaching events and ocean surface temperatures using a Geographic Information System (GIS). Point locations for coral bleaching events were overlaid on corresponding ocean surface temperature layers and temperature values were extracted to each bleaching location. This study found that 90.5% of bleaching events from 1985 to 2009 occur at temperatures above 26°C. When looking at bleaching events on a regional scale, between 50.0% and 94.8% of coral bleaching occurs at ocean temperatures above the regional average. Supporting previous research, this study found that 61.7% of all bleaching events from 1985 to 2009 occurred in the Caribbean. The results from this study show a global trend in bleaching events at higher than average ocean temperatures, reinforcing results from localized studies. Additionally, this study highlights the need to conduct additional research to understand why the Caribbean, one of the smallest regions, experiences a majority of the bleaching events. More research is required on reef mortality after bleaching events to be able to properly investigate coral adaptation to increasing temperatures. (**149**)

Krasik, Polina\*, Colleen Rattan\*, LenaRose DeLorenzo, and Jennifer Hayden Cedar Crest College, Allentown, PA 18104. Biofilm formation in Mycobacterium smegmatis is regulated by biofilm formation. - Lysine acetylation is a post-translational modification in which an acetyl group is covalently attached to a lysine side chain, changing the structure and function of the modified protein. While not as well-studied as other post-translational modifications, such as phosphorylation, lysine acetylation regulates a similarly large and functionally varied number of proteins. In bacteria, lysine acetylation plays a regulatory role in a number of important cellular processes, namely metabolism. Lysine acetylation is mediated by acetyltransferases, which add acetyl groups to lysine residues, and deacetylases, which remove the acetyl groups. In the soil bacterium, Mycobacterium smegmatis, the lysine acetylation/deacetylation regulatory system is comprised of one acetyltransferase, PatA, and one deacetylase, SrtN. We demonstrate here that biofilm formation in *M. smegmatis* is regulated by lysine acetylation. Specifically, overexpression of PatA leads to impaired biofilm formation. SrtN, on the other hand, is dispensable for biofilm formation. We also investigate the role of the lysine acetylation/deacetylation regulatory system on sliding motility. Mycobacteria do not have flagella, but show sliding motility on the surface of agar plates, a process that is linked to biofilm formation because both functions rely on the production of extracellular lipids. Since *M. smegmatis* serves as a model for the lung pathogen Mycobacterium tuberculosis, it is possible that lysine acetylation may regulate various bacterial processes necessary for infection, making it a potential new drug target. (9)

Kraycer, Paul\* Marywood University, Scranton, PA 18509. Krüppel-like transcription factor 3's effect on the insulin pathway using klf3::tph1 double mutants in the model organism Caenorhabditis elegans. — Obesity is a major health issue that has plaqued the U.S. for many years. Individuals that are obese have a higher risk of developing serious health complications like heart disease and type two diabetes. Some individuals have a predisposition towards obesity based on genetic factors that are not well understood. One group of genes that are related to obesity are the Krüppel-like transcription factors(KLFs). KLFs are transcription factors that have a distinct zinc finger domain at their C-terminus and play major roles in the human body from development to fat metabolism. Humans have a total of 17 KLFs which each have their own function within the cells. This can make studying their effects on different networks difficult. Therefore we study KLFs in the model organism Caenorhabditis elegans. Of particular interest is the klf3 gene which is homologous to the human klf1 gene and related to fat metabolism in the worms. Klf3 has been relatively well studied in respect to its effect and basic pathways, but there is a lack of data involving the insulin signaling pathway. The worms have a rudimentary insulin signaling system of proteins that mimics the same pathways as those in humans. One such protein is TPH1, which is related to increased fat storage, slower rates of egg laying, and slower rates of pharyngeal pumping. In order to test for genetic interactions between these genes we created

a *klf3::tph1* double mutant using RNAi microinjection. We observed a decrease in fecundity rates in double mutants as compared to *tph1* or *klf3* mutants alone. We also observed a decreased rate of pharyngeal pumping in double mutant worms, which indicates a possible genetic interaction between these two genes. (**53**)

Kunkel, David\*, and Grace Chen Misericordia University, Dallas, PA 18612. Effects of Periodic Drought on Delayed Seed Germination in Neotropical Costus Species. - Delayed seed germination in Costus villosissimus has been considered a drought escape strategy that facilitates the species' capacity to inhabit seasonally dry habitats along the edges of tropical rainforests (Chen 2011). Because C. villosissimus is predominantly isolated from its closely related, understory species, C. allenii, by their distinct habitats, environmental cues that break seed dormancy and trigger dermination can be key to local adaptation and speciation between the two species. We examined the effects of periodic drought on seed germination in C. allenii and C. villosissimus. Seeds were collected from the natural populations of the two species in central Panama in October 2016. Each seed was randomly assigned to one of the four germination treatments: control with consistent water availability, short, intermediate, or long drought with a 30-day water supply, followed by a drought period of 2, 10, or 30 days, respectively, and then a consistent water supply. The seeds were kept in a growth chamber with controlled temperature and day length mimicking the plants' natural environmental conditions. We found that C. villosissimus seeds, on average, germinated later than C. allenii seeds ( $81.30 \pm 5.61$  days and  $112.44 \pm 4.49$  days, respectively; p < 0.0001). Furthermore, C. villosissimus seeds under the control treatment germinated later than those in the drought treatments, while C. allenii seeds under the control treatment germinated earlier than those in the drought treatments (p < 0.0001). We conclude that the drought periods, regardless of their length, expedited seed germination of C. villosissimus but had a negative impact on the germination of C. allenii seeds. By investigating the adaptive mechanism of delayed seed germination, this study enhances our knowledge of local adaption and speciation in the tropics, where biodiversity is highly concentrated but speciation studies are relatively uncommon. (61)

Lamport, Samuel\*, and Mel Zimmerman Lycoming College, Williamsport, PA 17701. Prerestoration survey of Wolf Creek, an agricultural impaired stream in Lycoming County, PA. — The Lycoming County Conservational District is preparing to start restoration projects at 4 sites along Wolf Run in Muncy, PA. The restoration projects are needed because of the historical use of agriculture, limited or absent riparian buffers in the agricultural areas, conservation farming practices are limited, and there is a high rate of bank erosion. In 2013, the DEP completed a TDML (Total Maximum Daily Load) for the Wolf Run Watershed. In this document, the DEP recommended putting in: stream bank stabilizations, riparian buffers, and heavy use area protection, and manure storage. The project designed is going to stabilize 2.880 feet of stream bank and will prevent high amounts of nutrients and sediments from entering the Wolf Run Watershed. The Lycoming College Clean Water Institute Interns were tasked with completing a survey prior to the start of the restoration projects. This survey included, water chemistry, coliform sampling, fisheries survey, and macroinvertebrate samples were taken. The fisheries survey was only completed at the most upstream site. With the water chemistry data, we found that pH goes in a steady decline when going downstream, Alkalinity increases going downstream, and Orthophosphate and total Phosphorous both decrease going downstream. The fisheries survey showed that there were 9 species of fish present, and that the largest fish was 15cm in length. An Index of Biological Integrity showed biological imparment at all sites. The Lycoming County Conservational District is planning to complete the restoration in summer 2018. A discussion of project restoration BMP's and future monitoring will be made. (157)

**Lees, Nicole\*, and Jonathan Warnock** Indiana University of Pennsylvania, Indiana, PA 15705. *Determining the paleogeographical origin of the <u>Allosaurus Fragalis</u> from within the Cleveland Lloyd Dinosaur Quarry (Price, Utah) using biogenic apatite \delta180 values. — The Cleveland-Lloyd Dinosaur Quarry is part of the Morrison formation of eastern Utah and is death* 

assemblage dating to the late Jurassic. The CLDQ is a crucial site to understanding the dynamics within the Morrison formation. The quarry contains is the highest density of Jurassic bones discovered to date, with the highest allotment of bones belonging to *Allosaurus fragilis*. The quarry has an abnormally high ratio of predators to prey for a death assemblage. Unlike most predator traps, the CLDQ lacks a defined snaring mechanism, has a wide distribution of individual elements and has an imbalance between prey and predator, with a 3:1 ratio favoring prey. While multiple hypotheses have been put forward to explain the assemblage preserved at Cleveland-Lloyd, recent work suggests a component of both drought and flood processes created the deposit. We are analyzing the  $\delta^{18}$ O values obtained by processing the bioapatite from *Allosaurus* dentin, obtained from this location, to hypothesize their geographical origin. Since oxygen isotope values in vertebrate bone typically reflect the isotope values of the water they drink, similar values imply the *Allosaurus* are from a small geographic area, whereas disparate values would imply the *Allosaurus* were washed into the pond that the quarry represents from across a broad geographic area. (**47**)

Lehman, Kirstin\*, M. Dana Harriger, and Bradley Stiles Wilson College, Chambersburg, PA 17201. Investigation of possible points of contamination by Lactobacillus and Pediococcus in a microbrewery. - The number of microbreweries, breweries that produce a limited amount of beer, has grown 15 percent since 2015 and now makes up 12 percent of the beer industry, according to the Brewers Association. These breweries are growing in popularity all over the world due to their small batch sizes, attention to detail, and individualized flavor profiles; however, they are at increased risk for contamination by microbes due to limited resources and increased human manipulation of the product. This poses a problem economically because spoiled beer decreases profit. Brewing begins by malting grains, which are then boiled. After boiling, hops are added to the same tank. The liquid is then cooled and transferred to a fermentation tank, where yeast is introduced. After fermentation, the fluid portion goes to a conditioning tank, where it stays until bottling, kegging, or tapping. Lactobacillus and Pediococcus are Gram positive, anaerobic bacteria that most commonly spoil beer, making it unpalatable with an unfavorable aroma. These spoiling bacteria can contaminate the beer at multiple points during the brewing process. For this study, samples were collected throughout the brewing process, particularly at points of transfer within a local microbrewery: Roy Pitz in Chambersburg, Pennsylvania. Two beer products, a lager and an ale, were sampled. Samples were cultured in Hsu's Lactobacillus Pediococcus medium, an agar that inhibits the growth of yeasts and selectively grows Lactobacillus and Pediococcus at 37°C, for a total of three days. Lagers and ales require different processing temperatures; therefore, microbial growth in these two types of beer was of particular interest. The ability to identify any specific points of bacterial contamination would allow the brewer to evaluate existing protocols, enhancing the guality of their products. (116)

**LeMarble, Rachel\*, and Michael Foulk\*** Mercyhurst University, Erie, PA 16546. *Mapping putative amplicons onto larval salivary gland polytene chromosomes of <u>Sciara coprophila</u> using fluorescence <i>in situ hybridization.* — The fungus fly, *Sciara coprophila*, is known for its unique genetics, particularly developmentally regulated, locus specific gene amplification within the salivary gland giant polytene chromosomes. Subsequent transcription of the genes in these amplified loci results in the formation of DNA puffs. However, until recently comparatively little research utilizing modern genomic techniques investigating this phenomenon has been possible due to the lack of a high quality genome sequence. Fortunately, the *Sciara* genome has recently been sequenced and assembled. Moreover, multiple amplified loci were identified by sequencing the salivary gland DNA and mapping reads to the assembled scaffolds to identify regions with increased copy number relative to the surrounding sequences. Our current work focuses on the validation of the genome assembly by mapping the largest scaffolds to the giant polytene chromosomes using fluorescence *in situ* hybridization (FISH). In conjunction with this work, we are using FISH to map the hypothetical amplicons to a specific DNA puff in the polytene chromosomes. A sequence

specific probe was generated for each amplicon by PCR, then fragmented by limited DNasel digestion. This fragmented probe will then be labeled with fluorescent nucleotides and hybridized to the giant polytene chromosomes. Initially we are optimizing each step of the protocol using the best characterized DNA puff sequence at the II/9A locus. Once the protocol has been perfected it will be used to map the hypothetical amplicons. (77)

Levesque, Joshua\*, Margaret Garity, Elise Wetzel, and Jack Holt Susquehanna University, Selinsgrove, PA 17870. A multi-year study of diatom communities in the upper main stem of the Susquehanna River summer 2017. — The upper main stem of the Susquehanna River is formed by the confluence of the West and North Branch, both of which are chemically and physically distinctive and retain the signatures of the two branches due to weak lateral mixing. We refer to them as the West Branch plume (WBP) and the North Branch plume (NBP). Thus, characterization of the diatom communities requires samples taken from sites that occur in the plumes of both branches. Since 2009, we have monitored the upper main stem at an established transect that straddles Byers Island near Shamokin Dam, PA and below the Adam T. Bower inflatable dam at Sunbury, PA. Attached diatom communities were sampled from stones which were prepared for examination by scanning electron microscopy. The Pollution Tolerance Index (PTI) and Shannon Diversity Index (SDI) values showed very little variation between all sites (2.38-3.03 and 2.35-2.93). Sites were dominated by Discostella pseudostelligera (a small centric), Rhoicosphenia abbreviata (a biraphid), and Achnanthidium minutissium (a small monoraphid). Similar habitats of the WBP were dominated by Ach. minutissium and Encyonema appalachianum (a biraphid). Despite similarities between 2014 and 2017 regarding discharge, the diatom communities were depauperate this year (57 taxa; 104.470 cfs) compared to other high discharge summers (June, July, and August), especially 2014's. We found the greatest species richness in the diatom communities of the NBP (Site 3- 30; Site 4- 29). Proportional Bray-Curtis Similarity analyses of samples showed low to moderate overlap between the diatom communities. Across all sites we identified 57 different species. Differences in taxa richness could possibly be explained by effects of flushing during extended high discharge. (141)

Lokken, Britta\*, Kadeem M. Colburn, and Meg M. Laakso Eastern University, St. Davids, PA 19087. Investigation of an Emerging Outbreak: Fluorescent Tagging of Cotton Leaf Curl Gezira Virus. - Fiber crop scarcity has been exacerbated by the presence of the resistance breaking cotton leaf curl Gezira virus (CLCuGV) throughout Asia and Africa. Research identified viral genes of species in the same genus, Begomovirus, such as tomato yellow leaf curl virus, however, little is known of CLCuGV. Begomoviruses have six to eight genes, and putative roles have been assigned to V1 (coat protein), C1 (replicase), C2 (transcriptional activator). Studies have not identified a gene for movement protein in CLCuGV nor have researchers understood if multiple genes are associated with cell-to-cell transmission. Investigating  $\beta C1$ , C4, and V2 functions can confer characteristics of viral spread. We hypothesize that one (or more) of these genes control viral movement between host cells. To study viral movement  $\beta C1$ , C4, and V2 genes were isolated and fused at the cterminus to enhanced green fluorescent protein (eGFP) to create a cassette that could be visualized in infected cells. The cassettes were introduced singly into stable and transient vectors using standard cloning techniques and sequenced. Using Agrobacterium-mediated transformation, *BC1:eGFP*, *C4:eGFP*, and *V2:eGFP* were infiltrated into the first true leaf of the host, Abelmoschus sp. (okra), and non-host, Solanum lycopersicum (tomato). Using fluorescent microscopy, subcellular localization of the fluorescently-tagged viral proteins will be observed in vivo. Aniline blue staining will be used to identify plasmodesmata. The V1 coat protein is used as control, as it is known to traffic from the nucleus to the cytoplasm and does not associate with the plasmodesmata.  $\beta C1:eGFP$ , C4:eGFP, or V2:eGFP interaction with the plasmodesmata will support identification of movement protein(s). (33)

**Mabe, Lauren\*, Aubrey Ernest\*, and Megan Knoch\*** Indiana University of Pennsylvania, Indiana, PA 15705. *Effect of hyperglycemia on circadian rhythms in erythrocyte peroxiredoxins.* — Circadian

rhythms include any biological process that exhibits a sustained, regular oscillation over a 24-hour period. In the traditional view, a nucleus is needed to form a tightly controlled feedback loop with other parts of the cell in order to maintain the 24-hour oscillation. However, recent work has shown that red blood cells, which lack nuclei, exhibit robust circadian rhythms. This rhythm is caused by changes in oxidation of a protein called peroxiredoxin (PRX), which scavenges peroxides within cells. Diabetes is a metabolic condition that results from, among other factors, chronic high blood sugar. Recent research has shown that type II diabetes is closely tied to disruption of circadian rhythms in humans and mice. It is well documented that disrupted circadian rhythms influence the body's ability to metabolize glucose. Because high blood sugar can cause oxidative stress due to elevated hydrogen peroxide levels, we hypothesize that hyperglycemia can lead to disruption of circadian rhythms in red blood cell PRXs. To this end, we cultured red blood cells in high glucose media, sampled over a 24-hour period, and analyzed both peroxide and oxidized PRX levels to understand the effects of hyperglycemia on PRX rhythms. (51)

Macagnone, Anna\*, Nadia Namous, and Andre Walther Cedar Crest College, Allentown, PA 18104. Determining the Role of RPA Phosphorylation in Checkpoint Adaptation in the yeast <u>Saccharomyces cerevisiae</u>. - The uncontrolled cell growth seen in cancerous cells can be due to defects in the cell cycle checkpoints that are responsible for making sure that the cell divides with proper structural and genomic integrity. If DNA damage is recognized, the checkpoints lead to cellular arrest until DNA repair pathways can fix the damage. If the DNA damage is unrepairable, most cells maintain cellular arrest, which leads to apoptosis and cell death. Some single-celled organisms like the yeast Saccharomyces cerevisiaehave the alternative option of eventually releasing from the checkpoint and taking the chance of dividing with damaged DNA in hopes of repairing the damage in the subsequent phases of the cell cycle in a process called adaptation. The adaptation process in yeast is analogous to cancerous cells that continue the cell cycle in the presence of unrepaired DNA damage. Our research is focused on understanding the genes in S. cerevisiae involved in adaptation including KU70, DUN1, and Replication Protein A (RPA). We are particularly interested in RPA because it is phosphorylated in response to DNA damage, and we have previously shown that phosphorylation is required for adaptation. Using microdissection microscopy, we have observed adaptation in yeast strains containing combinations of mutations in RPA, KU70, and DUN1. Our results suggest genetic interactions between RPA, KU70, and DUN1 indicating that RPA plays an important role in cell cycle checkpoint adaptation. Using Saccharomyces cerevisiae as a model organism, this project intends to better understand the mechanism of adaptation that can provide insights in the growth of human cancerous cells. (106)

Manges, Anna\*, and Tom Simmons Indiana University of Pennsylvania, Indiana, PA 15705. Water mite parasitism of the Asian tiger and Asian bush mosquitos: vectors of West Nile virus and potentially Zika virus. - Manges, Anna and Simmons, Tom. Indiana University of Pennsylvania, Indiana, PA 15705. Water mite parasitism of the Asian tiger and Asian bush mosquitos: vectors of West Nile virus and potentially Zika virus - Larval water mite parasitism has been shown to reduce the fecundity and lifespan of adult mosquitoes, has been used to age-grade mosquitoes for management, and has been considered for biocontrol. A 2006 statewide study of mosquito-mite associations by IUP and the PA Department of Environmental Protection West Nile Virus Control Program documented 33 different associations, of which 17 were new to science. In 2016 after establishment of the Zika Virus Response Plan the PADEP collected and saved from destructive virus testing ten parasitized mosquitoes representing four species for which water mite parasitism was only rarely or not previously documented. These included an Asian tiger mosquito (Aedes albopictus) and an Asian bush mosquito (Aedes japonicus). Mites were removed, mounted, and identified using phase-contrast microscopy. Both Ae. albopictus and Ae. japonicus were parasitized by Parathyas sp. water mites, which represent the first and second North American records, respectively. (151)

**Marold, Joseph\*, and Avijita Jain** Indiana University of Pennsylvania, Indiana, PA 15705. *Synthesis, Characterization, Redox, and Spectroscopic Studies of a Tris(Heteroleptic) Ru(II) complex.* — Ruthenium (II) complexes containing polypyridyl ligands display highly versatile photophysical photochemical, and redox properties. Ru(II) complexes are interesting as photosensitizers as they possess reactive excited states that are easily tuned by modification of their ligands. Although sterically strained Ru(II) complexes containing two different types of ligands are reported in literature, the complexes with three different ligands are rare, due to the difficulty in synthesis. Herein, we report synthesis, characterization, redox properties, spectroscopic properties, and photoinduced ligand exchange studies of a new Ru(II) based tris-heteroleptic complex, [Ru(2,9-dmp)(bpy)](PF<sub>6</sub>)2, where 2,3-bis-2-pyridylpyrazine (dpp), 2,9-dimethyl-1,10-phenanthroline (2,9-dmp) and 2,2'-bipyridyl (bpy). (**167**)

Marotta, Julianna\*, and K. Joy Karnas Cedar Crest College, Allentown, PA 18104. Analysis of AcrAB-ToIC Efflux Pump overexpression in triclosan resistant Enterobacter spp. via quantitative PCR and expression cloning in Escherichia coli . - According to a report filed by the World Health Organization in January of 2018, the Global Antimicrobial Surveillance System has identified that 82% of blood stream infections are resistant to at least one commonly prescribed antibiotic. One potential cause for the uncontrollable spread of drug-resistant bacteria in many different environments is the overuse of antimicrobial agents such as triclosan, a bacteriostatic antimicrobial agent predominantly found in household hygiene and cleaning products. Initially developed to inhibit fatty acid synthesis in Gram-positive and Gram-negative bacterial species, triclosan provides a selective pressure for derived antibiotic resistance in a variety of bacterial species. Previous studies in our lab have indicated that Enterobacter cloacae and E. aerogenes strains resistant to triclosan show a concomitant increase in resistance to other antibiotics such as tetracycline and chloramphenicol. This study uses qPCR analysis via the comparative CT method to further investigate antibiotic resistance in these strains, demonstrating a potential connection between triclosan resistance and the up-regulation of efflux pump genes (AcrA, AcrB, and TolC) and associated transcriptional activator and repressor genes (MarA, MarR, OmpF). In addition, a Kirby-Bauer expression study focusing on the overexpression of E. cloacae efflux pump genes in IPTGinduced Escherichia coli T7 further correlates the impact of efflux pump gene overexpression on triclosan resistance. Future studies will focus on the impact of knocking out the AcrAB-ToIC efflux pump mechanism in Enterobacter and the expected downstream impact of this on triclosan and antibiotic resistance. Overall, these studies seek to better understand the function of the AcrAB-ToIC efflux pump as a mechanism for extruding antibiotics and chemicals from the cytoplasm of a bacterium and increasing microbial resistance to antibiotics. (117)

Marshall, Landry\*, and David Singleton\* York College of Pennsylvania, York, PA 17405. Subcellular localization of MNN4 tagged with green fluorescent protein in Saccharomyces cerevisiae. - Cell surface hydrophobicity (CSH) has been linked to play a significant role in enhancing virulence of pathogenic yeast by promoting adhesion to tissues. In Saccharomyces cerevisiae, and Candida albicans, deletion of the MNN4 gene resulted in the loss of cell wall phosphoryl mannose, which results in a decrease in CSH. It has been hypothesized that Mnn4p serves a regulatory protein involved with the addition of phosphate to the outer glycans of the cell wall, yet its exact function (i.e. enzyme or transcription factor) remains unknown. Activity of the gene has an effect on a process in the Golgi complex, however, protein sequence analysis of the Mnn4p protein suggest similarities with some transcription factors, and not with mannosyl transferases. The MNN4 gene product was tagged at the amino terminus and carboxy terminus with green fluorescent protein (GFP), in order to localize Mnn4p. Because the process of glycosylation occurs in the endoplasmic reticulum (ER) and Golgi complex, it is possible that Mnn4p activity will be seen in these structures. A GFP-URA3 linear plasmid was transformed into S. cerevisiae at the carboxyl terminus through homologous recombination. GFP was also cloned into a E. coli-yeast shuttle vector to drive expression from the amino terminus. Yeast transformants

were stained with DAPI, a fluorescent stain that binds to the cell's nucleus, and observed under fluorescent microscopy. The *MNN4* gene product emitted a green color, while the nucleus fluoresced blue. GFP was not localized to the nucleus suggesting that it does not play a role in regulation at the transcriptional level, but possibly functions as an enzyme that interacts with mannosyl transferases. Co-immunoprecipitation of Mnn4p and its potential binding partners would reveal what proteins it interacts with. (**158**)

Mauro, Colleen\*, Casey Markle\*, Daniel Straka, and Peter Smyntek Saint Vincent College, Latrobe, PA 15650. Hidden nutrient pollution: overlooked phosphate mitigation in a stream affected by abandoned mine drainage. — Abandoned mine drainage (AMD) and municipal waste water (MWW) are common, often coincident forms of pollution that impact streams in many regions of Pennsylvania (PA) and beyond. However, the impacts of these two types of pollution are often studied separately, and their interactions are not well documented in the field. Phosphate, which is one of the main nutrient pollutants in MWW, can react with or adsorb to iron and aluminum, the main metal pollutants associated with AMD in PA. This removes phosphate from the water column. Thus, AMD can potentially mask or mitigate the effects of phosphate pollution from MWW. As AMD remediation efforts continue, it is possible that previously hidden, underlying phosphate problems may emerge in areas that also have MWW discharges with high phosphate concentrations. This could lead to an excessive growth of algae and, in some instances, toxic algal blooms. To understand the magnitude of this hidden nutrient problem, phosphate concentrations as well as other water quality parameters were monitored at several sites during May/June and September/October 2017 in an AMD-impacted, second-order stream (4-Mile Run) that receives MWW inputs. Mixing ratios of AMD and MWW inputs to the stream, which were calculated using conservative ions (chloride and sulfate), indicated that 60 - 80% of phosphate from the MWW was rapidly removed from the stream. These high phosphate removal efficiencies demonstrate that hidden phosphate pollution is a large problem for this stream that must be mitigated in concert with AMD remediation. (152)

McCorkel, Olivia\*, Jody Teel, and Larry Corpus Misericordia University, Dallas, PA 18612. Survey of Macroinvertebrates in Container Habitats and Phytotelmata from Select Northeastern Pennsylvania Sites. - A Survey of Macroinvertebrates in Container Habitats and Phytotelmata from Select Northeastern Pennsylvania Sites - Many organisms, such as chironomids, mosquitoes, beetles, etc. breed in a variety of aquatic habitats. This study was conducted as part of a population survey of organisms that breed in container habitats, such as flower pots, litter, discarded tires, phytotelmata, etc. in select regions of northeastern Pennsylvania. In natural habitats, many of these organisms are very important ecologically, as they serve as prey for larger, more predaceous organisms. However, when containers become inundated with water, they serve as a relatively predator-free environment in which these organisms may flourish. Consequently, biological interactions, such as competition between mosquitoes and chironomids, may be magnified due to the close proximity and lack of predators. This study took into consideration these biological interactions in order to discuss the possibility of using biological control to reduce populations of container breeding pests, such as mosquitoes. Water samples were collected using a turkey baster and brought back to the laboratory to be identified, counted, and preserved. The results of the study suggest that there is a large presence of mosquitoes (3356) in these container habitats, with a lesser presence of chironomids (104), collembolans (31), mites (31), and other Diptera (10). The results do not suggest a decrease in the numbers of mosquitoes when in containers with high populations of non-mosquito macroinvertebrates. Further research should focus on collecting more samples from a greater variety of habitats in more regions of Pennsylvania in order to increase the sample diversity of container habitat organisms, and better determine if any biological interactions exist. (137)

McGee, Shannon\*, Constance Selinsky, Alexandra Morgan, Amy Reese, Lindsey Welch, Andre Walther Cedar Crest College, Allentown, PA 18104. *Analyzing different methods of physical*  agitation for the lipid extraction of Cryptococcus neoformans-Petroleum and other fossil fuels are non-renewable, and the combustion of fossil fuels contribute to global climate change. Biodiesel is a renewable, green energy source that burns cleanly and can replace fossil fuels; however, cannot currently compete against petroleum diesel in the economic market. Researchers have begun to study other sources of which to synthesize biodiesel from, to make a more cost effective product. Biodiesel is industrially synthesized by the transesterification of fatty acids from vegetable oils into their corresponding fatty acid methyl esters. Microbial biomass are an alternative source for biodiesel that are being researched that are capable of producing lipids. Cryptococcus neoformans is a widely studied organism due to its pathogenicity, and its entirely sequenced genome gives the option of genetic modification to increase lipid yield. The acapsular mutants that were studied have lost the pathogenicity that is linked to their capsule, and were therefore safer to work with in a laboratory setting. Between capsular and acapsular strains, acapsular strains were found to have higher FAME yields than capsular strains. C. neoformans strains were analyzed as the viable source for biodiesel production in this project. Currently, there is no agreement on standard optimized method or which method is best for lipid extraction from microbial biomass for the production of biodiesel. The main methods that were tested and compared are lyophilization, microwaving, bead-beating, and sonication as these are the most used methods in literature. The best method was a combination of lyophilization and microwave or bead-beating. There was no significant different determined using ANOVA between the microwave and bead-beating method. (175)

McLaughlin, Sean\*, and David Andrew Lycoming College, Williamsport, PA 17701. Automated analysis of spontaneous behavior in Drosophila melanogaster. - The Drosophila Genetic Reference Panel (DGRP) is a useful tool for identifying quantitative trait loci (QTLs) for complex traits in the fruit fly Drosophila melanogaster. Quantification of behavioral traits, however, can be prohibitively laborious as guantitative data analysis of videotaped behaviors can takes hours to analyze manually. Our study assessed the capabilities of the video-tracking software EthoVision XT® (Noldus Information Technology) to quantify spontaneous behaviors in flies. We proposed that EthoVision XT® would be able to accurately quantify the number and duration of walking and grooming bouts comparable to manually scored videos. Moreover, we aimed to use extracted data for both grooming and walking to analyze variation between the DGRP lines to perform genome wide association studies (GWAS) for identifying QTLs associated with these quantitative traits. We used video recordings of flies from the DGRP lines that had previously been scored manually for grooming behaviors to benchmark the settings for our automated software. These videos are of 24 hour-old flies that were placed in the wells of a 96-well plate and recorded for ten minutes of spontaneous activity. These videos were manually analyzed for four different behaviors: grooming, walking, standing, and falling. The number of grooming bouts and a grooming index were used to compare manually scored values against the output of EthoVision under various settings. Walking bouts were also compared in this manner. To compare manually and computationally scored values of these traits, we used geometric mean regression analysis to determine the similarity of measures. Our results showed that EthoVision was unable to adequately identifying grooming behaviors, but could extract walking behaviors from videos in a manner consistent with the more laborious manual scoring method. Future work will use the results of these analyses to perform GWAS analysis on spontaneous walking and grooming behaviors. (75)

**McMinn, Cutter\*, Hailey Shannon, Derek Wilson, Tara Barbarich, Brian Mangan, and Matthew Persons** Susquehanna University, Selinsgrove, PA 17870. *Variation in total mercury content of spiders from coal-impacted areas in Central Pennsylvania.* — Mercury is an important and persistent pollutant in the state of Pennsylvania but its transport across terrestrial and aquatic food chains is poorly understood. We measured mercury levels among spider taxa near various coal-impacted areas adjacent to or away from aquatic systems (N=904). Collecting sites from mining-

impacted areas included riparian zones and river islands adjacent and downstream from a former coal-fired power plant, upstream from a coal-fired power plant, the perimeter of a coal fly ash burial site, uncontrolled mine fire sites, and an AMD-impacted creek. Spider total mercury levels from these coal-impacted areas were compared to agricultural and headwater stream reference sites away from mining and coal burning areas. Mine fire sites had the highest mercury levels in spiders. Riparian zones just upstream of a powerplant had significantly lower mercury levels than downstream. Surprisingly, headwater streams had mercury levels as high as sites adjacent to the power plant. We also found significant differences in mercury levels among riparian spiders near the powerplant compared to agricultural sites. Mercury levels were unrelated to spider mass. Results indicate that ground spiders are particularly good bioindicators of mercury mobilization across aquatic and terrestrial interfaces within coal-impacted areas. Aquatic sources are important, but not necessary for significant trophic transfer among terrestrial arthropod predators since the mine fire sites had the highest mercury levels but were not in areas with significant water features. Spider size seemed to be a poor predictor of mercury levels among ground spiders suggesting that trophic level may not be adequately estimated by size alone. **(41)** 

**Melo, Mercy\*, Jean-Francois Therrien, and Allison Cornell** Cedar Crest College, Allentown, PA 18104. *Diet of American kestrels and its application as an alternative pest control system.* — American kestrels are one of the most abundant and widespread raptors in North America. By studying the diet of American kestrels at Hawk Mountain Sanctuary through inspection of pellets, three broad categories of prey could be identified: rodents, songbirds, and insects. These categories of prey all have a negative interference with various farming practices in Northeast Pennsylvania including contamination of grains, girdling of small trees and plants, consumption of farmed fruits, and defoliation of orchard trees. The introduction of American kestrels into regions of infestation or high concentrations of pests could help to limit these negative effects through their typical trophic interactions. By utilizing these natural interactions, farms would be able to limit the amount of artificial toxicants used and therefore avoid the poisoning of non-target wildlife. Artificial toxicants are also expensive to implement on large farms where many bait sites would have to be established. Attracting American kestrels would save farms time, labor, and profit margins by reducing or eliminating the amount of pest control needed to avoid crop damages. (**30**)

Michalides, Brandon\*, Seema Bharathan, and N Bharathan Indiana University of Pennsylvania, Indiana, PA 15705. Analysis of mycoviral dsRNA in Rhizoctonia solani isolates 303, 357, 386 using CRISPR. - Rhizoctonia solani is a soil-borne pathogenic fungus with distinct isolates classified based on their anastomosis groups (AG's). Previous studies from our lab have shown that isolates of these fungi contain M-size double-stranded viral RNA (dsRNA) that are generally cytoplasmic and viral in origin. A full- length of dsRNA was synthesized using the conventional RT-PCR FLAC method and was cloned into vector and sequenced. The aligned ORF maps for ORFs of translated sequences have significant homology to those of known genes for mycoviral capsid proteins. The blastp alignments indicated that each sequence contained at least one ORG with significant homology to a known R. solani dsRNA coat protein, with noticeable low E value scores. The DELTA-blast searches for the homologous ORFs yielded multiple "hits" with viral coat proteins from Red clover and White clover cryptic viruses. Attempts are currently being made to clone these genes into mammalian expression vectors and optimize using optimization software from GeneArt. Data from sequence verification of coding region will be optimized. These viral dsRNA plasmid clones of *R. solani* were picked from culture grown in a medium containing ampicillin. Using Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR), attempts were made to knock out genes of ampicillin resistance in some of these clones. We plan to use this as a model system for work using CIRSPR guided genome edition of viral coat protein gene cloned from mycoviral dsRNA infecting R. solani. (88)

**Mikeasky, Noriko\*, and Cuong Diep** Indiana University of Pennsylvania, Indiana, PA 15705. *Using CRISPR-Cas9 to create a yeast strain for genetic screens.* — Kidney disease affects approximately

15% of the U.S. population and current therapies have severe limitations. Therefore, an alternative therapy is urgently needed. Humans cannot regenerate new kidney tissue, but zebrafish can. They do this using specialized stem cells that express the *lhx1a* gene. Recently, we showed for the first time that *lhx1a* dimerized in a genetic assay. Deleting the LIM domain of *lhx1a* enhanced dimerization. Others have also shown that deleting the LIM domain activated *lhx1a*, making it a constitutive transcriptional activator. Thus, we hypothesize that *lhx1a* dimerization may be important for its activation. This provides a new mechanistic model for how *lhx1a* activity is regulated. For this reason, it is important for us to determine the dimerization domain of *lhx1a*. In this project, the CRISPR-Cas9 system is used to create a new yeast strain expressing the LexA (op)-URA3 reporter. This new strain will be used for genetic screens to identify *lhx1a* mutants that fail to dimerize, which could lead to mutation hot spots at the dimerization domain. Understanding the molecular mechanism of *lhx1a* may lead to the manipulation of kidney stem cells for enhanced kidney regeneration. (**102**)

**Mills, Rachel\*, Krista Silvis\*, Colin Berkheimer, Tessa Woods, and Edward Levri** Penn State University-Altoona, Altoona, PA 16601. *The effect of habitat type on the growth and reproduction of the invasive New Zealand snail.* — The invasive New Zealand mud snail (*Potamopyrgus antipodarum*) has been established in North America for over three decades and is well-established in the Greater Yellowstone Ecosystem. In Polecat Creek, Wyoming, it exists in extremely high densities in multiple habitats. In its native New Zealand, the snail varies in density and life-history characteristics by habitat within the same water body. The purpose of this study is to determine if there are differences between New Zealand mud snails inhabiting different habitats within Polecat Creek. Here we compare three different life-history characteristics between New Zealand mud snail populations within three different habitats (stream bank, reeds, and macrophytes). Snails were sampled using a dipnet from each habitat. Each snail's length was measured and was dissected to determine if brooding offspring. If brooding, the number of offspring was recorded. A preliminary analysis of the data suggests that the snails grow to a greater length and produce larger brood sizes in the reed habitat compared to the others. These results suggest that habitat type may influence the invasion success of this species. (**143**)

Minnig, Patrick\*, and David Osgood Albright College, Reading, PA 19604. Evaluation of <u>Microstegium vimineum</u> success under varying timber management techniques. - In 2013, the Department of Conservation and Natural Resources initiated forestry management at Nolde Forest State Park outside of Reading, PA. Three sites were managed, each with a different forest management technique (clear-cut, select-cut, salvage-cut), opening up the opportunity to analyze the effects of these different techniques on the succession within the plant community. Disturbances within the plant community are known to open up opportunities for invasive species to establish themselves. *Microstegium vimineum* (Japanese Stiltgrass) is a dominant invasive grass at Nolde forest. We established 4 randomly placed quadrats in each site and quantified diversity within the plant community for these quadrats in each of the five study years. Soil samples (annually) and *M. vimineum* clip plots (2 years) were also collected for analysis of soil and foliar nitrogen and aboveground biomass. There were no significant differences among sites (P = 0.0711, ANOVA), but there was a trend of higher M. vimineum biomass at two of the three disturbed sites (clear-cut and salvage-cut) relative to the control and the third disturbed site. M. vimineum success correlated with plant cover and canopy cover, but not soil nitrogen or plant community metrics. Despite the significant increase in biomass over the past 5 years, M. vimineum did not appear to be regulating soil nitrogen in any significant way. M. vimineum success was facilitated by a combination of openings in the forest canopy and forest floor, allowing for M. vimineum to quickly establish itself probably due to its C4 qualities. The disturbance is likely causing *M. vimineum* biomass to increase, primarily in relation to sunlight, however it is still too early to tell if these differences can be attributed specifically to disturbance type. (60)

Mong, Hannah\*, Yuval Silberman, and Jessica Petko Pennsylvania State University- York, York, Pennsylvania 17403. Beta-2-adrenergic receptor expression changes in stressed mice. — The betaadrenergic receptors belong to a class of G protein-coupled receptors that are activated by the endocrine signals, epinephrine and norepinephrine. These signals serve to generate anxiety-related behavioral changes throughout the body. While the key pathway studied in stress responses is the hypothalamic-pituitary-adrenal axis (HPA axis), various brain structures including the amygdala (known for its roles in fear and emotional memory) feed into the HPA axis to modulate responses. Recently our collaborator has shown that mRNA levels for the Beta-2 subtype of adrenergic receptor (B2AR) is elevated in the amygdala of acutely stressed mice, and that this increase in transcript is associated with enhanced signaling and neural activity. In this study, we aimed to examine two possible explanations for increased expression of B2AR: altered methylation of promoter DNA and potential binding of nuclear receptor transcription factors. We hypothesized that methylation would be unaltered by acute stress, while binding of the glucocorticoid receptor (nuclear receptor for the stress hormone cortisol and corticosterone) to B2AR enhancer regions would be increased. Methylation analysis was performed by bisulfite conversion of genomic DNA from mice that were either unstressed or stressed by 1 hour of restraint. No differences in methylation have yet been detected between stressed and control mice. In the next phase of our study we will measure the binding of the glucocorticoid receptor to enhancer regions near the B2AR gene by chromatin immunoprecipitation analysis. (80)

Morales, Millina\*, and Stephanie Justice-Bitner Kings College, Wilkes-Barre, PA 18711. Resistance to lavender oil (Lavandula angustifolia) in Serratia marcescens. - Resistance to lavender oil (Lavandula angustifolia) in Serratia marsescens. Serratia marcescens is a gram-negative bacterium known to be a common cause of hospital acquired infections as it is both hardy in hostile environments and widespread. Additionally, this bacterium is difficult to combat as it is highly resistant to some antibiotics. Essential oils have been found to be a reliable defense against pathogenic bacteria. These oils are comprised of a combination of mainly terpenes and phenols that allow them to attack the cell walls of gram-negative bacteria. Lavender oil (Lavandula angustifolia) has exhibited antimicrobial activity against many species of pathogenic bacteria and have been found to work against some clinical drug resistant bacteria. The fight against bacterial resistance is a continually evolving field of research as it needs to keep up with the rate at which the bacteria itself build resistance against previous treatments. The natural inhibition many essential oils have against bacteria opens the field up to new potential treatment options as well as possible future conjunctions between current antibiotics and compounds derived from essential oils that could lead to a major decrease in the buildup of bacterial resistance. In this study, a strain of Serratia marcescens was able to acquire complete resistance against lavender oil in nine generations of exposure through disk diffusion. (12)

**Moser, Erin\*, Darin McNeil, and Jeff Larkin** Indiana University of Pennsylvania, Indiana, PA 15705. *Dynamic habitat associations of <u>Bombus</u> in early-successional forests of northern Pennsylvania.* — Bumble bees (*Bombus* spp.) play an essential ecological role within the northeast United States and beyond. Especially important for crops that require 'buzz pollination', *Bombus* and other native bees are attributed with 3.07 billion dollars per year in agricultural gross domestic product. However, like other bee species, *Bombus* are experiencing declines across the North American continent. These declines are thought to be driven by a variety of factors including pesticide use, exotic disease, and habitat loss. Though *Bombus* are relatively well-studied in agricultural systems, understanding of their ecology within native forest ecosystems remains almost entirely unknown. Moreover, the extent to which habitat management through silviculture benefits eastern bees remains unknown. To begin filling these knowledge gaps, we conducted an observational study across two heavily-forested counties of Pennsylvania (Clinton and Centre). In 2017, we conducted line transects through n=48 recently-managed forests, with each transect repeated three times. We then used hierarchical distance models to estimate detection probability and true *Bombus* density (bees/km<sup>2</sup>) as a function of habitat. We found that detection probability varied as a function of wind and density varied as a function of a variety of habitat features. Density models for habitat indicated selection for shrub cover but avoidance of sapling cover. Our interaction data suggested that *Bombus* relied mainly on flowering shrubs and herbaceous forbs during the sampling period. Dynamic patterns of habitat association appeared to be driven by plant bloom cycles with flowering shrubs selected most heavily during *Vaccinium* and mountain laurel (*Kalmia latifolia*) bloom and *Rubus* avoidance after its flowering period. Increasing densities of *Bombus* were recorded from period 1 (30.3 workers/ha) to periods 3 (127.49 workers/ha). Densities reported here are higher than the densities reported by many past studies highlighting the importance of early successional forests, and thus benefit of forest management, to pollinators like *Bombus*. (**36**)

**Mukherjee, Sujata\*, and Robert Major** Indiana University of Pennsylvania, Indiana, PA 15705. *Identifying tbx20 as a Pattern Regulator During Planarian Regeneration.* — The inability to repair aging or damaged tissues is a strong contributor to disease. The freshwater planarian flatworm, containing a pluripotent stem cell population, has an incredible capacity to regenerate every cell type in its body, making it an excellent model system to unlock the pathways governing injury-induced tissue repair and maintenance. My study explores the role of a transcription factor, Tbx20, as a patterning regulator. I have cloned a large fragment of the planarian *tbx20* gene and have performed RNA interference to knockdown its function during regeneration. Regenerating fragments exhibit an abnormal posterior indented blastema where medial tissues fail to regenerate. As these phenotypes are only present in the posterior-facing blastema, and in more posterior regions of the animal, I propose that *tbx20* coordinates anterior-posterior and medial-lateral axes during regeneration. My studies on *tbx20* function will provide information on how axial patterning in the planarian during tissue regeneration. **(71)** 

**Muller, Rebecca\*, and Akeisha Belgrave** Harrisburg University of Science and Technology, Harrisburg, PA 17101. *Relating bacterial cell wall synthesis to bacterial antibiotic susceptibility in rod-shaped cells.* — Rod-shaped bacteria increase in length without significant change in width. The ability to maintain a rod-shape during growth can be attributed to the cell wall or peptidoglycan (PG) layer in the cell. During cell growth, PG units are synthesized in the cytoplasm and transported to the PG layer for insertion. To ensure the successful insertion of new PG material, a protein complex through a known mechanism makes room in the existing cell wall by severing peptide crosslinks, inserting new material, and re-crosslinking. Cells that replicate faster have less crosslinked cell wall material. To test whether there is a relationship between bacterial crosslink density and antibiotic susceptibility, *Escherichia coli* N698–a strain with imp4213 deletion and a resulting permeability of the outer membrane–was treated with Vancomycin and its morphology and antibiotic susceptibility was monitored at varying replication rates to simulate varying levels of crosslink density in the cell walls. The results indicate a negative relationship between crosslink density and Vancomycin induced cell death. (6)

**Munir, Gina\*, Rebeccah Bailey\*, Summer Arrigo-Nelson, and Paul Nealen** Indiana University of Pennsylvania, Indiana, PA 15705. *Activity budget and mating behaviors in zoologically housed siamang gibbons (<u>Symphalangus syndactylus</u>). — Despite their prevalence in zoological institutions, to date there is no long-term record or analyses of the siamang (<i>Symphalangus syndactylus*) activity schedule or behaviors in a zoological setting. Without this detailed information it is impossible to properly identify signs of lethargy and stereotypic behaviors, which could be signs of disease or stress. In addition, despite their endangered status, little research exists on breeding behaviors of the siamang in the wild or in captivity. The purpose of this study was to monitor a breeding pair of zoo-housed siamangs, at the Pittsburgh Zoo and PPG Aquarium, to determine if siamangs exhibit specific mating patterns/behaviors and a visibly discernable estrus cycle. We observed a sexually mature male-female pair over a span of 6 weeks. The pair was video recorded two days each week, continuously for one hour, either in the morning or late afternoon, in their indoor exhibit. These

videos were scored to construct a preliminary ethogram and activity budget for each individual. Then, an additional fifteen hours of video was collected and scored for assessment of mating and breeding behaviors. The activity budget comparisons revealed that captive siamangs spent most of their time brachiating while indoors, and, while there was no visual indicator of an estrus cycle in the focal female, it appears that male attentiveness to the female (e.g., playful chasing and close proximity) may foreshadow mating attempts. Additionally, it was determined that copulation in captive siamangs mirrors that in the wild, with males approaching females to copulate dorsoventrally and participating in suspensory copulation. Further study is needed to determine if these behaviors persist as the pair becomes older and more sexually experienced. We hope that this study improves the basic understanding of captive siamang mating behaviors, and contributes to the success of future siamang breeding efforts. (**39**)

Namous, Fadia\*, and Andre Walther Cedar Crest College, Allentown, PA 18104. Examining the role of Replication Protein A phosphorylation's genetic interactions with other checkpoint genes in regulating the cellular response to chemotherapeutic drugs in Saccharomyces cerevisiae. - Cancer is among the leading causes of death worldwide and the number of new cancer cases will rise to 22 million within the next two decades therefore there is a dire need to understand this disease. The budding yeast Saccharomyces cerevisiae has been widely used as a model organism to understand the underlying causes of cancer because of the significant level of homology in cell cycle and DNA maintenance pathways. This research is focused on the highly conserved, single-stranded DNA binding protein Replication Protein A (RPA). RPA plays central roles in DNA replication, DNA repair, cell cycle control, and telomere synthesis, which are pathways often dysfunctional in human cancerous cells. RPA is phosphorylated in a cell cycle dependent manner and in response to DNA damaging agents suggesting a possible role in regulating the cellular response to DNA damage. It has been previously shown that RPA phosphorylation plays a role in allowing yeast cells to survive in the presence of DNA damage. The goal of our research is to elucidate the role of RPA phosphorylation in regulating genetic pathways responsible for responding to different DNA damaging chemotherapeutic drugs including: camptothecin, phleomycin, and hydroxyurea. Each of these DNA damaging agents induces DNA damage in a unique way that can be used to understand the interaction these drugs have with the genes being studied. We will present results showing that mutants with rfa2-Asp, when a cell is engineered to behave like it is always phosphorylated, are less sensitive than the wild type, which can be phosphorylated and dephosphorylated in a cell cycle dependent manner, on Phleomycin. A better understanding of RPA's role in each of the DNA repair and cell cycle pathways and how it interacts with other genes will allow researchers to understand some of the underlying causes of cancer and assign better agents to selectively target cancer cells. (107)

**Namous, Nadia\*, and Andre Walther** Cedar Crest College, Allentown, PA 18104. *Examining the Role of RPA phosphorylation in the Telomere Synthesis pathway in* <u>Saccharomyces cerevisiae</u>. — Cancer is the second leading cause of death in the USA, and is caused by uncontrolled cell division of cells within the body. Replicative immortality is one of the hallmarks of cancer that is due to the activation of telomerase in cancer cells. Replication Protein A (RPA) which is a highly conserved heterotrimeric single stranded DNA binding protein that is involved in DNA replication, recombination, repair, and telomere synthesis. The second subunit of RPA can be phosphorylated, and phosphorylation affects its function in the cell. The focus of this project was to understand the genetic interactions between RPA and the proteins known to involved in the telomere synthesis pathway and understand how phosphorylation of RPA affects these interactions the model organism *Saccharomyces cerevisiae*. In addition, the telomerase pathway is always active in yeast cells, so they can be comparable to cancer cells because in cancer cells, the telomerase pathway becomes activated which enables them to regenerate telomeres and replicate continuously. Several of the genes involved in the telomere regulation model such as *EST1, PIF1, RIF1, TEL1, KU70*, were deleted in yeast strains containing mutations that led to constitutively phosphorylated or

unphosphorylated RPA. The genomic DNA from each strain and was extracted and the telomere length was analyzed using a PCR method to specifically amplify telomeric DNA. Data suggests that phosphorylated RPA strains seem to have shorter telomeres than unphosphorylated strains using the PCR method. (**108**)

Nevin, Andrew\*, and John Harms Messiah College, Mechanicsburg, PA 17055. Implicating gastrin signaling in K-ras-mediated tumorigenesis. - Gastrin is a peptide hormone with important functions in regulating digestion; however, it has also been implicated in pancreatic tumorigenesis. Elimination of gastrin from pancreatic ductal adenocarcinoma (PDAC) has been shown to greatly decrease tumor growth. K-ras is an important oncogene, mutated or activated in multiple cancers, including lung, colon and 90% of pancreatic cancers. Previous studies have demonstrated that when a mutant, oncogenic K-ras allele (G12V) was introduced into near-normal. non-tumorigenic, human pancreatic ductal epithelial (HPDE) cells, H6c7, the H6c7-Kr cells exhibited 50% tumorigenicity and showed altered expression of 43 different genes. We have hypothesized that K-ras mediates its tumorigenic effects through gastrin, among other effectors, and sought to elucidate a connection between K-ras and gastrin in early tumorigenesis. We have shown gastrin mRNA is present at very high levels in both H6c7 and H6c7-Kr cells. However, the gastrin receptor, CCK2R, is upregulated in H6c7-Kr cells, indicating receptor abundance may contribute to the shift in tumorigenicity. To confirm the relevance of this change, we treated H6c7 and H6c7-Kr cells with two CCK2R antagonists (proglumide; YM022). When gastrin signaling was blocked, both lines showed a marked decrease in growth rate regardless of K-ras status. A decrease in gastrin RNA in both lines also suggests inhibition of an autocrine signaling loop driving the elevated gastrin expression and growth rate. Thus, K-ras activation may impact gastrin signaling and cell proliferation through upregulation of the CCK2R and, at minimum, autocrine augmentation of existing, aberrant gastrin expression. (111)

Parente, Amy\*, Miguel Garcia-Rubio, and Michael Healy Mercyhurst University, Erie, PA 16546. Creation of a wireless sensor network to gather real-time temperature, pH, and conductivity data from remote locations. - Wireless sensor networks (WSNs) have become a large part of a technologically-based society and have a multitude of uses ranging from Internet of Things (IoT) applications and militarized functions to environmental and habitat research. We have created a wireless sensor network using Vernier-brand products and other inexpensive commercial-off-theshelf (COTS) parts and materials. The three main components for this wireless sensor network are the remote nodes, a gateway node, and the monitoring station. Each remote node measures several different environmental parameters (pH, temperature, and conductivity for this study), using separate probes which are housed in a waterproof casing to allow for their introduction into the environment. The gateway node gathers the data from the remote nodes and through an internet connection relays this information back to the monitoring station (our lab at Mercyhurst University). Calibration of the remote nodes has been completed in our lab, and data from a simulated field study has demonstrated the ability of this system to reliably provide real-time 24/7 environmental data from multiple remote locations. This WSN will be introduced to several local aquatic environments during the Summer 2018 months to gather data for several ongoing research projects studying water quality issues in the northwest region of Pennsylvania. (65)

**Parker, Shane\*, and Jonathan Warnock** Indiana University of Pennsylvania, Indiana, PA 15705. *The effect of a Western Antarctic Ice Sheet collapse on nutrient recycling rates during marine isotope stage 31: Initial findings.* — Expedition 177 of the International Ocean Discovery Program yielded valuable cores from the Southern Ocean. Site 1094, taken southwest of the tip of Africa in the circum-Antarctic opal belt, contains a span of time in the Early Pleistocene (roughly 1 million years ago) that covers the marine oxygen-isotope stage 31, a hypothesized period of West Antarctic Ice Sheet collapse. This study evaluates the taphonomic condition of *Fragilariopsis kerguelensis*, the most common diatom in Southern Ocean sediment, recovered from this site as a proxy for nutrient recycling in the upper water column. The core depth (~118m-123m below the

seafloor) includes a time interval before, during, and after the collapse. By cataloguing morphological dissolution of this prevalent diatom, links between the collapse and subsequent release of nutrient rich sediments and upper water column nutrient cycling can be evaluated. Additionally, the effects of a dissolved silica influx to the tropics, known as silica leakage, will be addressed. (**156**)

Perez, Alexis\*, Stephanie Justice-Bitner, and Barbara Fenner Kings College, Wilkes-Barre, PA 18711. Glutamate exposure causes transposition of phosphatidylserine to the outer plasma membrane in SH-SY5Y cells. - Neurodegenerative diseases, like Parkinson's and Alzheimer's diseases, are characterized by a progressive loss of neurons in specific regions of the central nervous system. The cause of degenerative diseases very, but they share common pathological features: oxidative stress, inflammation, and apoptosis. Microglia, the phagocytic cells in the brain, are activated in neurodegenerative diseases. Once activated, microglia secrete inflammatory proteins that may damage neurons. Once neurons are damaged, they transpose phosphatidylserine (PS) from the inner to outer membrane of the cell. This acts as a signal that the cell is stressed and enhances phagocytosis of that cell. This PS transposition is reversible, and will reverse when the cell recovers from the stressor. If the cell does not recover, apoptotic pathways will be activated and the cell will die. Glutamate, the major excitatory neurotransmitter, can induce excitotoxicity in pathological conditions, and is therefore used to injure neurons in many in vitro models of degeneration. The purpose of this study is to determine if glutamate-inducedexcitotoxicity causes PS transposition in the plasma membrane of SH-SY5Y cells. Annexin, a phospholipid-binding protein, conjugated to FITC was used to detect the amount of "flipping" that occurs after treatment with various concentrations of glutamate. Future studies will address whether neurons expressing PS are preferentially phagocytosed by microglia. (57)

**Phillips, Taylor\*, and Stephanie Justice-Bitner** Kings College, Wilkes-Barre, PA 18711. Using the *Kirby Bauer method to examine bacterial resistance to tea tree essential oil.* — Antibacterial resistance is a growing threat to human health. Due to the increase of resistant strains of bacteria, alternative substances that contain antimicrobial properties are being investigated. Essential oils are derived from angiosperms; and they contain properties that have been shown to kill bacteria. Some of these properties include hydrophobic composition and chemicals which include terpenes and phenols. Bacteria used in the study include *Staphylococcus aureus, Escherichia coli,* and *Enterobacter aerogens.* To induce resistant bacteria, lawns were plated, and sterile discs were impregnated with oil which was added to the plate. The zone of inhibition was measured and satellite colonies were selected and were used to grow the next generation. This process was carried out for eight generations in triplicate. Inhibitory zones decreased in diameter with each generation, indicating that bacteria can become resistant to the antimicrobial compounds found in tea tree oil. (**13**)

**Phung, Lan-Nhi\*, and Michael Foulk** Mercyhurst University, Erie, PA 16546. *FISHing for amplicons: mapping hypothetical amplified loci to the giant polytene chromosomes of* <u>Sciara</u> *coprophila* by fluorescent in situ hybridization. — The fungus fly, Sciara corprophila, is a genetically unique organism, yet there is still little knowledge about its genome. During the late stages of larval development, the DNA in the salivary gland undergo repeated rounds of replication (up to 13) without intervening cell division. The resulting copies remain synapsed together creating giant polytene chromosomes. At 18 loci of these giant polytene chromosomes, an isolated origin of replication fires repeatedly resulting in localized amplification, providing more template for transcription of the genes at these loci . Subsequent transcription of the genes creates visible "DNA puffs". One of these loci (II/9A) has been extensively studied, but little is known about the other DNA puff sequences. A draft genome assembly of of the *Sciara* genome has recently been produced and sequencing of the salivary gland DNA revealed the sequence of the other DNA puff loci. However, it is still unknown whether these hypothetical amplicons actually exist in the *Sciara* genome or to which DNA puff each sequence cooresponds. Here we present experiments designed to localize these amplicons to the giant polytene chromosomes. This project attempts to map one hypothetical amplified locus to the polytene chromosomes of *Sciara* to confirm its existence, determine from which DNA puff the sequence derives, and map its location in the genome. Our protocol includes extraction of DNA from the salivary glands, PCR amplification of the amplicon sequence to generate a probe fragement, fragmentation of this probe and the labeling of the probe with fluorescent dyes. This probe will subsequently be hybridized to the polytene chromosomes using fluorescence *in situ* hybridization (FISH) to localize its position in the *Sciara* genome. (**78**)

Pomopsello, Michelle\*, and Kara Mosovsky Moravian College, Bethlehem, PA 18018. The effect of the dietary antioxidant Seleno-L-Methionine (SeMet) on Burkholderia thailandensis infected macrophages. - Intracellular bacterial infections are difficult to treat because most antibiotics are unable to penetrate into mammalian cells. Prior research on intracellular infections suggests treatment with the cytokine interferon gamma in combination with the antibiotic ceftazidime yields significant Burkholderia thailandensis killing in a macrophage infection model. We believe the combination treatment uses a mechanism of action to kill bacteria that relies on the production of excess reactive oxygen species. In order to confirm this hypothesis, this study explored the effect that the antioxidant Seleno-L-Methionine (SeMet) had on the macrophages and bacteria. Trypan blue exclusion was used to determine the percentage of live macrophages after they were treated with SeMet at varying concentrations. SeMet was toxic to macrophages at a 1000 uM concentration. An in vitro infection model was then used to observe the effect that SeMet had on infected macrophages. In contrast to uninfected cells, macrophages that were infected and treated with 1000 uM SeMet appeared healthy, and also had less bacterial burden than the untreated controls. Surprisingly, this high SeMet concentration resulted in a similar intracellular bacterial burden compared to our successful combination therapy of antibiotic and immune stimulant, though it did not add to the effect when combined with the combination therapy. This concentration of SeMet was determined to inhibit bacterial growth on its own. Contrary to our hypothesis, these results suggested that the antioxidant is helping to control the infection, at least in part, by inhibiting bacterial growth. Further research is required to understand the mechanism of action that both the antioxidant SeMet and combination treatments use in order to inhibit intracellular infection. (119)

**Rachii, Diana\*, Elizabeth Skendzic, and Edward Sambriski** Delaware Valley University, Doylestown, PA 18901. *Analysis of anthocyanins in fruits.* — Anthocyanins are a group of photoprotective plant pigments of very diverse chemical structure. Due to the health benefits associated with anthocyanins, their demand in food and dietary supplements has significantly increased. Therefore, a variety of studies are focused on finding inexpensive and effective methods of quantitation, separation, and identification of anthocyanins. The objective of this study was to separate and identify anthocyanins in nine fruit samples: black and red grapes, plum, red pear, blackberry, strawberry, eggplant, black olive, and cherry. *Delphinium* and green pear were used as positive and negative controls, respectively. Thin Layer Chromatography (TLC) with various combinations of stationary and mobile phases was used for pigment separation and UV-visible spectrophotometry was used for pigment characterization. Quantification and identification of specific types of anthocyanins were not attempted as they require expensive standards, however, the shift in wavelength due to variation of anthocyanin structure was observed and discussed. The pH dependent change in color was also analyzed and light microscopy was used to localize accumulation of anthocyanins in the fruit cells. (**169**)

**Ratliff, Maria\*, and Emily Basile** Cabrini University, Radnor, PA 19087. *Using the biomarker glutathione S-transferase (GST) in arthropods to measure aquatic ecosystem health.* — Glutathione S-Transferase (GST) is a bioindicator that can be used to examine the health of an ecosystem, as GST activity has been found to fluctuate in the presence of xenobiotics in the environment. Using a biomarker may provide a more sensitive evaluation of the ecosystem health than the more common

measurements of physical properties of water such as a Water Quality Index (WQI), or the biological communities such as a Biotic Index (BI). In this study, two sites with varying levels of human disturbance were sampled along Crabby Creek in Eastern Pennsylvania. Westlake Drive (WLD) was the more impacted ecosystem compared to Crabby Creek Park (CCP). Based on site assessments, it was hypothesized that the GST activity would be less in CCP compared to WLD. To test this hypothesis, GST activity was evaluated using a Quantichrom<sup>™</sup> GST Assay kit in the amphipod from suborder Gammaridea. GST activity in CCP was found to be higher compared to WLD. The contradictory results may suggest the amphipods could have evolved resistance to the chronic exposure to pollutants at WLD, explaining the lower levels of GST activity compared to CCP. Other possible reasons for the contradictory results include, variations of GST activity in an organism due to fluctuating temperature, time displaced from the tested environment and reproductive output. These factors were not accounted for in the experiment. Furthermore, potential problems with the assay include the use of glutathione past the recommended use date and not homogenizing the organisms to a complete extent. Future studies should be done considering these factors as they may influence the results. Overall, the biomarker GST did prove to be a more sensitive test compared to the WQI and BI which found no difference in guality between the two sites. (131)

**Reisinger, Katherine\*, and Thomas Cook** Mercyhurst University, Erie, PA 16546. *Correlation between toxic releases and low-income neighborhoods.* — Low-income, minority communities have been historically and disproportionately exposed to environmental health hazards. Certain industrial facilities in the U.S. must report to the EPA annually how much of certain chemicals are release onand off-site. The purpose of this project is to use ArcGIS to examine correlations between community characteristics and exposure to pollution emissions. This research will include spatial analysis examining air pollution emissions and toxic release from industrial facilities who report to the EPA Toxic Release Inventory (TRI), to see whether low-income communities are disproportionately exposed to known carcinogents. The focus is primarly on three toxic cheicals released in the air that are known to pose a major threat ot human health and the environment. In 2016, OSHA carcinogen air releases were primarily releases of styrene (44% of the air releases of all OSHA carcinogens), acetaldehyde (13%), and formaldehyde (8%). The research will look first at data for the entire state of Pennsylvania and then focus in on Erie County. Income data will be drawm from the Census. (135)

**Replogle, Kirsten\*, and Lindsey A. Welch** Cedar Crest College, Allentown, PA 18104. *Hydrogenation of a-methyl-trans-cinnamaldehyde using metal chloride additives.* — The compound a-methyl-trans-cinnamaldehyde is often used in fragrances and flavorings. It also serves as a model compound for selective hydrogenation. Results of the investigation of the hydrogenation of this compound using Pd/C in isopropyl alcohol (IPA) and hydrated metal chlorides will be presented. The hydrated metal chlorides used were FeCl<sub>3</sub>·6H<sub>2</sub>O, SnCl<sub>2</sub>·2H<sub>2</sub>O, CuCl<sub>2</sub>·2H<sub>2</sub>O, and NiCl<sub>2</sub>·2H<sub>2</sub>O. Reactions were carried out both at atmospheric pressure using a hydrogen balloon and at high pressure in a Parr microreactor. Progress was monitored with GC/MS and GC/IR. Catalytic transfer hydrogenation was observed at high pressure in IPA. Hydrogenation activity was enhanced in the presence of Pd/C, but metal chlorides were able to facilitate hydrogenation in the absence of Pd/C. Decarbonylation was a favored pathway over hydrogenation, and may have been caused by the steric hindrance around the olefin group. Comparison of these results to those of cinnamaldehyde may explain the mechanism of hydrogenation for these aromatic aldehydes. Reaction pathways predicted will be compared to current literature. (**174**)

#### Rhyder, Nikell\*, Eric Martine\*, Helana Supsic, Jonah Winakor, and David

**Richard** Susquehanna University, Selinsgrove, PA 17870. *Reproductive success and ovarian gene expression in <u>Drosophila melanogaster</u> maintained in a simulated high altitude (low-pressure) environment.* — Global surface temperatures have been rising steadily over recent centuries, largely due to anthropogenic CO<sub>2</sub> emissions, and are extending the potential habitat ranges of insect disease vector populations into higher altitudes. While a number of investigations have examined

the effect of low oxygen levels on development and gene expression, we are unaware of any that have examined this using air at low pressure rather than via novel gas mixes. We exposed newly eclosed fruit flies (Drosophila melanogaster) to a low-pressure environment equivalent to an altitude of approximately 6,000m above sea level in a custom-built hypobaric chamber. This altitude approximates the highest permanent human habitations in the Himalayas, an area where climate change is having profound effects. The chamber was housed at 25°C in a photoperiod of L12:D12 to examine the effects of hypoxia due to low pressure on ovarian development; a control group was maintained under the same conditions at ambient pressure (sea level). Ovaries were removed 36h post eclosion and examined for size and the extent of egg development. The ovaries are now stored in RNAlater® for subsequent RT-PCR analysis of the expression of hypoxia inducible factors and those genes involved in yolk protein synthesis and trafficking. Our investigation revealed no difference in ovarian length or width attributable to the low-pressure environment at this temperature (p=0.933 and 0.871 respectively) indicating at least tentatively that these environments are a possible habitat for invasive insect populations. Similar experiments to determine fecundity and reproductive timing of *Drosophila*development under these and other conditions are ongoing. (69)

Rifflard, Deborah\*, Deborah Austin, and M. Dana Harriger Wilson College, Chambersburg, PA 17201. The effects of probiotics on canine weight and fecal fat content. — Obesity is a global and a national epidemic that affects nearly 37% of U.S. adults. According to the National Institutes of Health (NIH), obesity is now the second leading cause of preventable death in the U.S. and is responsible for an estimated 300,000 deaths per year (2015). Obesity is a metabolic disorder that has a variety of causes, however the most common is an imbalance of energy intake and expenditure. Obese adults are predisposed to developing a number of diseases such as cardiovascular disease, type 2 diabetes, hypertension, and osteoarthritis. These adults may also experience a decreased lifespan and an overall lower quality of life. Studies in animals and humans have demonstrated that the gut microbiota and several metabolic disorders, including obesity, have a positive correlation. Restoring the beneficial microbiota population by adding probiotics into one's diet may aid in weight loss. In this study, a controlled population of whippets from the Wilson College Veterinary Medical Center were utilized to minimize breed variables. All dogs were housed in the same environment, fed the same diet, and received the same amount of daily exercise. The initial weights of the dogs were recorded. Fecal samples were analyzed using the Van de Kamer method to establish baseline fat content. A probiotic capsule was administered to the treatment group once a day at the morning feeding for thirteen consecutive weeks. The weights of the whippets and the fat content of fecal samples were determined every two weeks for five months. Preliminary results suggest that weight loss can be achieved by taking a probiotic pill and that age affects fatty acid content in feces. Probiotics may provide a possible naturopathic treatment alternative that is non-invasive and cost-effective for the control of obesity in humans. (120)

#### Romani, Isabella\*, Jenna Bucca, Bailey Babarsky, Andrew Conboy, and Melinda

**Harrison** Cabrini University, Radnor, PA 19087. *Discover and annotation of novel bacteriophages: lilboat and inspire2.* — Bacteriophages are viruses that infect a bacteria host, potentially leading to strategies for treating, preventing, or diagnosing bacterial infections such as tuberculosis that are resistant to conventional antibiotics. We have discovered two novel siphoviridae type phages named Lilboat and Inspire2 from the *Arthrobacter* sp.ATCC 21022 host. Both phages were purified from soil samples and their genomic DNA isolated. After isolating the genomic DNA, they were photographed through the use of an electron microscope and then the DNA was sequenced. Phage Inspire2's genome was then annotated using various bioinformatics tools, such as DNA Master; Phamerator; HHpret and GeneMark to determine gene location and function. Using comparative genomics, unique characteristics of the phage's genome were also explored. (7)

**Ross, Ayla\*, and Josiah Townsend** Indiana University of Pennsylvania, Indiana, PA 15705. *Mitochondrial phylogeny of highland frogs (Anura: Ranidae: <u>Rana maculata</u>) from Nuclear* 

*Central America.* — Central American frogs are easily misidentified using solely morphological data, confusing conservation efforts by incorrectly assessing threats impacting individual populations. Phylogenetic analysis offers a supplemental identification tool, specifically the use of mitochondrial and nuclear genes to determine if two related groups are of the same population or if they consist of two or more species. This study examines one such species, *Rana maculata*, and provides a preliminary estimate of phylogenetic relationships among populations of *R. maculata* based on a fragment of the gene 16S. Analysis of 72 samples recovered five distinct lineages within *R. maculata*, most of which occur in isolated locations. Further analysis of additional genetic data as well as morphological data and bioacoustics should be used to resolve the taxonomy of this group. This data will help narrow conservation efforts compared to a wide-spread single species to preserve these small endemic populations. (44)

Sakyi, Edmund\*, and Karl Kleiner York College of Pennsylvania, York, PA 17405. The effect of Tree of Heaven (Ailanthus altissima) on the growth and soil fungal community of Black Locust (Robinia pseudoacacia). - Ailanthus altissima is widespread in 48 of the 50 states in the USA. Removal of *Ailanthus* using fire, chemicals and mechanical means are expensive and ineffective. If Ailanthus cannot be removed physically from the environment, we must determine if other plant species are able to co-occur and grow alongside Ailanthus. Ailanthus is a known allelopath that chemically inhibits the growth of surrounding plants by releasing the chemical compound ailanthone into its surrounding environment. The allelopathic effects that stems from Ailanthus may operate by influencing the soil microbial species and may not have a direct impact on other species. Black Locust (Robinia. pseudoacacia) is an early successional tree species that shares the same habitat requirements with Ailanthus. We asked if Ailanthus had an allelopathic effect on black locust and if so, whether Ailanthus did so through altering the soil fungal community. R. pseudoacacia were grown alone and paired with Ailanthus. Ailanthus and R. pseudoacacia were grown from seed in the York College Navlor Ecological Sciences Center greenhouse. Biolog FF microplates were used to assess the functional richness and diversity of the soil fungal community. The mass of the roots and shoots of the black locust in paired and individual pots were not significantly different from each other. The functional diversity, functional evenness, functional richness, and turbidity development were not significantly different between paired and unpaired treatments. The number of *Rhizobia* nodules on the roots of *R. pseudoacacia* was significantly less when grown in paired pots with Ailanthus. Our results indicate that R. pseudoacacia is unaffected by the presence of Ailanthus because the growth and fungal community of R. pseudoacacia were not significantly impacted when grown alongside Ailanthus. Overall, if R. pseudoacacia can grow alongside Ailanthus, then more attention can be focused on discovering additional plant species that can co-occur with Ailanthus. (32)

**Samuel, Dressler\*, Rosa Rodriguez, and Mary Morrison** Lycoming College, Williamsport, PA 17701. *Role of the PI-3 kinase pathway in Purkinje cell dendrite development.* — The cerebellum is the part of the brain responsible for coordinating motion and balance. Within the cerebellum, Purkinje neurons integrate information about location and movement of body parts in space and time. The Purkinje cells then send output signals back to the brain to adjust the control of motion and allow for smooth and precise movements. Cerebellar Purkinje cell dendrites collect this information and Purkinje cell axons send these signals to the deep cerebellar nuclei. The morphology of these neurons partially determines their function. Neurotrophins, such as brain-derived neurotrophic factor (BDNF), are known to regulate Purkinje cell growth, differentiation, and function. This study manipulated the signaling pathways downstream of BDNF receptors in cultured cerebellar neurons and examined the effects on cell body size, dendritic branching, and dendrite length. Using the MetaVue computer software, we measured the effect of a neurotrophic inhibitor at varying concentrations on the parameters of Purkinje cell dendrite development in cerebellar cell cultures grown for 14 days. This study specifically observed the inhibition of the PI-3 Kinase pathway, which is known to be downstream of BDNF signaling. We hypothesized that

inhibition of this signaling pathway would interfere with Purkinje cell development by limiting dendritic outgrowth. Inhibition of the PI-3 Kinase pathway did not alter the length of the longest Purkinje cell dendrite, but significant decreases in cell body, total cell, and dendritic area were observed. Manipulations of these signaling pathways could lead to treatment options for future patients with neurodegenerative diseases caused by improper Purkinje cell morphological development. (98)

**Santarelli, Jeremy\*, Dan Cooney, and Quyen Aoh** Gannon University, Erie, PA 16541. *Role of SCAMP3 in*  $\beta$ *-Amyloid Production and Secretion.* — Alzheimer's disease is a neurodegenerative disease associated with loss of memory and cognitive function. The aggregation of extracellular plaques containing  $\beta$ -amyloid is related to the processing of the amyloid precursor protein (APP). The degradation of APP is regulated by the endosomal sorting complexes required for transport (ESCRTs) and disruption of ESCRT function leads to accumulation of B-amyloid. Previous studies have shown that secretory carrier membrane protein 3 (SCAMP3) interacts with ESCRTs that function in APP processing. We hypothesize then that SCAMP3 functions in trafficking of APP. In this study, I will use a well-established ELISA assay to determine if RNAi-induced knockdown of SCAMP3 promotes or inhibits  $\beta$ -amyloid production. (101)

Schell, Joseph\*, and Howard Whidden East Stroudsburg University, East Stroudsburg, PA 18301. Documenting the distribution of eastern small-footed bats (Myotis leibii) in the Delaware Water Gap National Recreation Area. - Eastern small-footed bats (Myotis leibii) have traditionally been considered one of the rarest bat species in northeastern North America and they are listed as threatened or endangered in several states, including Pennsylvania and New York. However, there is still much that is not known about the population status and summer roosting ecology of this species. This lack of information may stem from the eastern small-footed bat's habitat preference of rocky outcrops and talus slopes, which are scattered and difficult to survey, as well as survey methods that may be ineffective for this species. We used three techniques to survey for eastern small-footed bats in the Delaware Water Gap National Recreation Area in eastern Pennsylvania and western New Jersey: active acoustic monitoring, stationary acoustic monitoring, and visual searches for roosts. We selected five sites of suitable habitat in the Delaware Water Gap National Recreation Area and surveyed over the summer and fall of 2017. We then used occupancy modeling to compare detection probabilities for the three techniques. Eastern small-footed bats were detected at three of the five sites. Active acoustic monitoring was the most effective technique at documenting this species (detection probability of 0.25), followed by stationary acoustic monitoring (0.18), and finally visual roost searches (0.08). In a similar study in Virginia, visual roost searches were most effective at detecting this species, whereas acoustic monitoring was least effective. This difference between studies may be due to the type of detectors used for acoustic monitoring and the learning curve associated with visual roost search surveys. (127)

**Selinksy, Constance\*, Alexandra Morgan\*, and Andre Walther** Cedar Crest College, Allentown, PA 18104. *Optimization of liquid media and carbohydrate sources for biodiesel fatty acid production in mutant strains of the oleaginous yeast <u>Cryptococcus neoformans</u>. — Fossil fuels such as coal, natural gas, and crude oils supply roughly 81% of the energy that is consumed each year in the United States, but these fuels are in finite supply and their combustion is harmful to the environment. Knowing the tolls of burning fossil fuels has led to an increased effort to find alternative fuels sources that are cost efficient, as well as clean burning. The major goal of this project is to use microorganisms such as oleaginous yeasts in the production of high levels of lipids that can be converted to biodiesels. Researchers have studied the oleaginous fungus <i>Rhodoturula sp.* that produces a fair amount of lipids and is easy to grow. In this project, we are using *Cryptococcus neoformans* as a model organism to produce lipids and have shown that lipid production is higher in *C. neoformans* than in *Rhodoturula sp. Cryptococcus neoformans* is a valuable yeast to investigate because its genome if fully sequenced and has well developed genetic engineering tools that are not available in *Rhodoturula*. Our experiment shows not only comparable,

but better lipid yield than what has been seen with *Rhodoturula*. Our current research is focused on examining growth analysis with strains of *Cryptococcus neoformans* containing mutations affecting capsule and lipid metabolism, and identifying alternative carbohydrate sources such as, lignin, xylose, mannose, malt extract, glycerol, and cellulose, to find a much cleaner and cost-efficient sugar than dextrose. The aforementioned glycerol is an interesting route of study because one of the waste products from the chemical extraction process of lipids is glycerol. We have shown that glycerol can be extracted from a solution that matches our waste products with minor contamination. Taken together, our research indicates that *C. neoformans* may be a strong model organism that can be used to produce lipids for biodiesel production. (**26**)

Semenkow, Melissa\*, and Jessica Nolan York College of Pennsylvania, York, PA 17405. The impacts of fishing practices on aquatic basking turtles within Lake Marburg. — There is a warm water fishery for a number of species in Lake Marburg (Hanover, PA), including largemouth bass, bluegills, catfish and yellow perch. Fishermen have reported catching turtles on their fishing hooks and being unable to remove the hook from the turtle's mouth, which may cause injuries. The purpose of this study was to determine which fishing baits aquatic basking turtles within Lake Marburg are most attracted to and whether vision or olfaction plays a larger role in the turtle being able to find its food. A combination of a field study and a controlled laboratory experiment was used to complete this experiment. In the field, aquatic turtles were trapped using corn, chicken liver, and worms. The chosen bait by the each turtle was recorded. In the lab, vision or olfaction was impaired to determine which sense was more important in finding and choosing a food. The bait that the turtles chose and the time to locate the bait were recorded. It was found that painted turtles (Chrysemys picta) and musk turtles (Sternotherus odoratus) preferred corn and chicken liver compared to worms in the field. It was also found that both vision and olfaction were important to peninsula cooters (Pseudemys peninsularis) when finding and choosing bait in lab. Fishermen are advised to use dead worms as bait to lower the amount of turtles caught on fishing hooks. (148)

Shafto, Theresa\*, Courtney Gehman, William Holl, and Erin Ventresca Albright College, Reading, PA 19604. Quantification of diadzein binding to the estrogen-related receptor in Drosophila Melanogaster. — Drosophila melanogaster, the common fruit fly, are a vital model organism for many areas of study, including hormone signaling. Drosophila undergo a welldocumented molting process during their larval development that is dependent on the ecdysone hormone signaling pathway. Previous studies demonstrated that after Drosophila larva were fed different sov products, there was an increase in larval death during these molting stages. We hypothesized that a particular component of the soy contained a possible hormone causing the premature larval death. Due to its homology to the estrogen receptor, we hypothesized that binding of phytoestrogen compounds, isoflavones, to the estrogen-related receptor (ERR) may be responsible for this lethality. Using flies expressing a transgene containing the ERR ligand binding site fused to a GAL4 driving GFP expression we were able to directly visualize whether ligand binding to the ERR ligand binding domain occurred. When Drosophila were fed differing amounts of the isoflavones diadzein and genistein in yeast paste, there was significant GFP expression in response to the diadzein indicating a direct binding relationship between the diadzein and the ERR. This fluorescence was not seen when the Drosophila were fed the genistein suggesting that the isoflavone binding may be diadzein-specific. Using ImageJ we were able to quantify this data to determine the significance of diadzein concentration and location of receptor binding to compare to our larval survival studies. (74)

**Shaible, Tierney\*, Avery Russell, and Tia-Lynn Ashman** University of Pittsburgh, Pittsburgh, PA 15260. *Microbes shape pollinator preference.* — Pollinator preferences drive flower display evolution. Flowers with preferred traits are visited more, which further increases selection for preferred traits. Microbes living on flower surfaces might alter the flower display (e.g., by producing scent cues), and thereby affect pollinator preferences. We therefore assessed whether microbes on live flowers can act as a cue for bees, shaping both innate and learned preferences. We used

greenhouse grown *Exacum affine* flowers, the bumble bee, *Bombus impatiens*, and a supplementary microbial community (composed of 2 known bacteria and 2 known yeast). To determine the quantity of microbes to add to flowers used in this experiment, we counted the number of microbes on flowers of five different plant species, collected along a 4.5 km long transect in Pittsburgh. We assessed bees' innate preference by presenting flower naïve bees with an array of two types of flowers: flowers supplemented with microbes in solution and flowers supplemented with a control solution. To assess whether bees could learn a preference for one of the flower types, bees were trained to either microbe supplemented flowers or control solution supplemented flowers, and then tested in an array composed of both flower types, alternated by position. We found that flower-naïve bees strongly avoided flowers supplemented with microbes. Bees which were trained to one of the two flower types showed a learned preference for the experienced flower type 1 hour later during the testing period. Our results indicate that flower microbes are yet one more cue bees can use to discriminate among flowers. Our results also suggest we should expect flowers to evolve traits that reduce persistence of cue-providing microbes and, simultaneously, that microbes should evolve to evade pollinator perception. (27)

Shannon, Hailey\*, Brynn Hainey, Tristan Campbell, and Matthew Persons Susquehanna University, Selinsgrove, PA 17870. The effect of single and multiple predator cues on survival, foraging and antipredator responses of the wolf spider, Pardosa milvina. — The wolf spider Pardosa milvina shows effective antipredator behavior in the presence of chemical cues from the cooccurring predatory wolf spider, Tigrosa helluo. The "threat-sensitive predator avoidance hypothesis" predicts that, because of the costs associated with antipredator behavior, animals should allocate defensive responses proportional to the perceived threat. The wolf spider Tigrosa helluo is syntopic with Pardosa milvina and represents a chronic daily predation threat. The fishing spider, Dolomedes tenebrosus is allotopic and will consume Pardosa but, because of microhabitat preferences in less likely to encounter Pardosa. Tigrosa facultatively burrows and hunts on the ground but ineffectively from vertical surfaces while Dolomedes may occupy and hunt from vertical surfaces more commonly. We used differences in these species space use and encounter frequencies with Pardosa to independently manipulate perceived predation risk and measure Pardosaresponse to silk and excreta cues produced by these predators. We measured variation in Pardosa response (freezing) to chemical cues produced from either Dolomedes, Tigrosa, or both species simultaneously. We also manipulated the location of these predator cues on vertical or horizontal surfaces resulting in nine predator cue treatments in all combinations of prey cue location (side or bottom), species (Dolomedes or Tigrosa), and number of predator cues used (one or two) (n=30, N=270). We also quantified the foraging costs and survival benefits of such behaviors. Tigrosa attacked and preyed on Pardosa more than twice as often as Dolomedes. Pardosa showed greater reductions in activity in the presence of Tigrosa cues. The presence of *Tigrosa* cues on the ground significantly impaired foraging but also significantly increased Pardosa survival when in the presence of a live predator. Overall we found broad support for the threat-sensitive predator avoidance hypothesis. (42)

**Showers, Jeannie, Margaret Blaetz, Christopher Pagan, and Ellen Yerger** Indiana University of Pennsylvania, Indiana, PA 15705. *Influence of Plot Location on Common Garden Outcome for Measurement of Leaf Herbivory.* — Common garden plots provide a homogenous growth environment, allowing direct comparisons of treatment effects. In this study our treatments were different plant species, with the aim of comparing insect herbivory levels on the leaves. Our objective was to determine if insect herbivory differences are responsible for the astounding differences in plant success of native and non-native plants. This study compared invasive honeysuckle leaves, *Lonicera morrowii*, to its native congener *L. sempervirens*, and also compared invasive multiflora rose leaves, *Rosa multiflora*, to its native congener *R. carolina*. The plants missing leaf area was measured for each species. Even though each plot location was planted in an identical common garden design, our results show widely varying herbivory. For honeysuckle,

insects removed less leaf area from invasive plants growing in our Natural Area plot, more in our Farm plot, and the same as native plants in our Suburban plot. This suggests that the location of the plot, and the surrounding ecosystem, has more of an effect on the insects feeding activity than the plant species. (49)

Slappo, Jessica\*, Kelsey Twining, Gregory Mount, David Janetski, and Michael Tyree Indiana University of Pennsylvania, Indiana, PA 15705. Ecological recovery from acid mine drainage in passive remediation ponds in western Pennsylvania. - Acid mine drainage is a pervasive problem in the United States, with 14,763 miles of contaminated streams across the country and 9,396 miles in the Appalachian region. Passive treatment of mine drainage typically involves forcing water through a series of ponds to neutralize pH and capture heavy metal precipitates, but monitoring of biological recovery seldom occurs. To assess recovery attained by passive treatment systems, we measured macrophyte density and diversity, as well as macroinvertebrate community composition at two ponds in the Tanoma treatment system, located in western Pennsylvania. Results showed a correlation between macroinvertebrate composition and pond location, with 55% more sensitive taxa present near the outlet pond. Vegetation density was 3.4 times higher in the outlet pond than in the pond closer to the raw mine discharge. Our findings show that water quality improvements from passive treatment systems permit substantial ecological recovery from the harmful impacts of abandoned mine discharge. Treatment systems with engineered ponds and water level controls may be effective for use in other regions where heavy metal remediation and biological restoration are desired. (146)

**Smithbauer, Michelle\*, Maureen Levri, and Edward Levri** Penn State University-Altoona, Altoona, PA 16601. *The effect of floral height on pollinator visitation in Mountain Laurel (Kalmia latifolia*). — Mountain laurel (*Kalmia latifolia*) produces different numbers of inflorescences and flowers per inflorescence on each plant every year. Previous work has shown that in mountain laurel inflorescence size increases with height off the ground, and there may be a reproductive advantage to having inflorescences higher on the plant. To test the hypothesis that higher flowers lead to greater reproductive success, we examined the pollinator visitation rate on flowers at different heights. We used about 5 flowers high on a plant and 5 flowers low on the same plant on each of 23 plants and determined how many anthers were manipulated by bumblebee pollinators at one day and two days after the flowers opened. A preliminary analysis of the data suggests that in mountain laurel, flowers higher on the plant are visited more by pollinators. This suggests that the greater reproductive investment observed in higher inflorescences may result in greater reproductive success. (37)

Soto, Samantha\*, and Josiah Townsend Indiana University of Pennsylvania, Indiana, PA 15705. Species delimitation of Smilisca baudinii. - Species delimitation of Smilisca baudiniiThe family Hylidae is the most diverse and well-studied fauna of tropical amphibians (Smith 2006). It has a total of 861 species and 42 genera (Smith 2005). This family ranges over North, South, and Central America and follows the oldest known pattern of ecology and biography: that species richness increases from pole to equator. The most recent biogeographic and excepted hypothesis of this family, is the Middle American clade. This clade includes all endemic species to North and Central America. The Middle American Clade then divides into four smaller clades that include the Smilisca, Triprion, and Anotheca clade (Faivovich 2005). The Smilisca genus (Cope 1865) consists of eight total species that inlcude: S. baudinii, S. cyanostiota, S. dentata, S. fodiens, S. phaeota, S. puma, S. sila, and S. sordida. The purpose of this project is to access the species level-taxonomy of the common Mexican Treefrog Smilisca baudinii. Originally found in Mexico with restriction to Cordoba, Veracruz (Duellman 1968) S. baudinii is found from southern Texas to Costa Rica and is found in and around human habitation (IUCN 2010). Despite the abundance of this species, little taxonomic evolutionary research has been done on this species over the past 50+ years, therefore it has been untouched by modern genetic techniques. Recently, DNA sequences for 33 samples of S. baudinii from Honduras and Nicaragua were generated in the Townsend Lab, and surprisingly

revealed that there may be as many as three species masked by this name, in those two countries alone. The objective of this project is to analyze the available comparative genetic data and a preliminary phylogenetic hypothesis. The results of this project will form the foundation for an expanded study across the entire range of the species. (**125**)

**Spadafora, Sonia\*, Bailey Babarsky, Isabella Romani, and Melinda Harrison** Cabrini University, Radnor, PA 19087. *Discover and annotation of a novel bacteriophage copper.* — Bacteriophages are viruses that infect a bacteria host, potentially leading to strategies for treating, preventing, or diagnosing bacterial infections such as tuberculosis that are resistant to conventional antibiotics. We have discovered a novel AN cluster siphoviridae type phage named Copper from the *Arthrobacter* sp.ATCC 21022 host. Phage Copper was purified from a soil sample and its genomic DNA isolated. After isolating the genomic DNA, it was photographed through the use of an electron microscope and then the DNA was sequenced. Phage Copper's genome was then annotated using various bioinformatics tools, such as DNA Master; Phamerator; HHpret and GeneMark to determine gene location and function. Using comparative genomics, unique characteristics of the phage's genome were also explored. (8)

Stambaugh, Samuel\*, Nicole Clemente, and Lawrence Mylin Messiah College, Mechanicsburg, PA 17055. Cryopreservation of human erythrocytes for laboratory culture of Plasmodium falciparum. - Malaria is caused by five species of the parasite *Plasmodium* and primarily affects people living in third-world countries who often do not have effective means or funds to control the parasite. One such area is Zambia where the most lethal form, Plasmodia falciparum is most prevalent. Our current work is intended to support ongoing malaria research at the Macha Research Trust (MRT) [also known as the Malaria Institute at Macha (MIAM)], which is located in Macha in the Southern Province of Zambia. Laboratory cultivation of Plasmodium falciparum requires fresh human blood. It is difficult to assure the constant supply of fresh, uninfected human blood needed to sustain culture experiments because blood from local residents cannot be used, and because many visiting scientists and physicians routinely take a prophylactic anti-malarial drug that also makes their erythrocytes unable to support propagation of *Plasmodium* in culture. Cryopreservation of red blood cells obtained from uninfected individuals in the US with subsequent shipment to Zambia is an option we are investigating. Our goal is to learn to freeze fresh, leukocyte-depleted erythrocyte suspensions using minimal aqueous volumes of a macromolecular starch-based cyroprotectant. Hydroxy ethyl starch (HES) and polyvinyl alcohol (PVA) have shown promise as ice recrystallization inhibitors (IRIs) which prevent ice crystal formation during the thawing process. This presentation will describe our attempts to: determine appropriate concentrations for use of these IRIs; identify appropriate freezing, thawing and storage conditions; and characterize the ability of cryopreserved RBCs to support asexual propagation and/or gametocyte formation for the Plasmodium falciparum laboratory strain NF54. (52)

**Steber, Clay\*, Allison Peeney, and Nicole Chinnici** East Stroudsburg University, East Stroudsburg, PA 18301. *Prevalence of <u>Babesia odocoilei</u> infections in Pennsylvania elk – Babesia odocoilei* is a tick-borne protozoal parasite that infects the erythrocytes of members of the family Cervidae. This study aims to examine the prevalence of *Babesia odocoilei* infections in harvested Pennsylvania elk. A total of 190 blood samples from harvested Pennsylvania elk were submitted by the PA Game Commission. Samples were analyzed using a nested PCR reaction specific for *Babeisa odocoilei* and positive PCR samples were confirmed with DNA sequencing. Results indicated 26 percent of elk were infected with *Babesia odocoilei*. *Babesia odocoilei* infection can cause hemolytic anemia and mortality within elk populations. Due to the isolated nature of Pennsylvania elk populations they are at high risk for population decline. (**122**)

**Stern, Sydney\*, and Sheryl Fuller-Espie** Cabrini University, Radnor, PA 19087. *In vitro anticancer effects of protein extracts from <u>Eisenia hortensis</u>: A flow cytometry study investigating inhibitory actions on a colon cancer cell line. — Thousands of years ago earthworms were used by the* 

Chinese to treat dozens of illnesses including bronchitis, ulcers, and cancer. Studies have proven that earthworms have proteins that mediate protective mechanisms similar to those executed by mammalian phagocytes and natural killer cells. Since most cancer treatments are nonspecific and detrimental to healthy cells, research is being conducted investigating the use of earthworm extracts as a potential method for cancer treatment. In this study, earthworm protein extracts were collected from Eisenia hortensis, purified, and fractionated using ammonium sulfate cuts. Gel electrophoresis demonstrated that different collections of proteins were obtained depending on whether 35% or 50% ammonium sulfate was used. Induction of apoptosis in a cancer cell line derived from the cecum of a patient with Duke's type B colorectal carcinoma was investigated using the purified protein extracts. Apoptosis was measured using annexin-V-FITC and flow cytometry. Significant increases in apoptosis were observed with both protein fractions showing a correlation between percent apoptosis and treatment dosage. Using an RNAseA/propidium iodide cocktail, cell cycle analysis was also performed to determine if the earthworm protein fractions were capable of interfering with cell cycle phases of the cancer cell line. In one of two trials, significant increases in the G1/G0 phase and decreases in the S phase of the cell cycle were observed in treated compared to untreated cancer cells. Future analysis needs to be conducted including a non-cancerous human cell line as a control instead of the hamster and monkey cell controls used in this study. Gentler cell harvesting methods could serve to reduce the high levels of apoptosis observed in baseline samples. Finally, additional purification of the crude extracts is necessary to elucidate which proteins are mediators of apoptosis and inhibitors of DNA synthesis in the colorectal carcinoma cell line used in this study. (109)

Stoneberg, Kelsey \*, and Kimberly Johnston Delaware Valley University, Doylestown, PA 18901. Amplification of Oncorhynchus nerka COI gene from PIT tag trocars as a potential new field analysis technique. - Salmon are an important species to the ecosystem in the Pacific Northwest. Many salmon species are declining in number because of man-made dams and salmon ladders that block their migration. Whooshh Innovations™ has designed a fish transport system that assists fish over dams and salmon ladders, potentially reducing energy expenditure and allowing the fish to travel further upstream to spawning grounds. Several studies are ongoing to determine whether the Whooshh<sup>™</sup> system is a better alternative to ladders. The general design of these studies is: fish are trapped, PIT tagged (passive integrative transponder), and a tail punch taken for species identification. The PIT tag allows Whooshh™ to track the fish as they travel upstream through PIT tag arrays. Studies have indicated that tail punching may be detrimental to the fish as they travel upstream. PIT tagging leaves an empty trocar that potentially contains tissue from the tagged fish. The purpose of this project was to determine whether enough tissue remains in the used trocar for DNA extraction and sequencing for species identification. This would allow for the elimination of the tail punch. Primers were designed for amplification of the COI gene. DNA was extracted from fresh frozen samples of Sockeye Salmon (Oncorhynchus nerka). The COI gene was amplified by PCR followed by sequencing and bioinformatics. Used PIT tag trocars were analyzed for the presence of tissue. Mock PIT tagging determined that enough tissue remains in the used trocars for DNA extraction. A timepoint analysis determined that there is approximately a ten-fold reduction in DNA every 24 hours. Therefore, used trocars should be immediately immersed in lysis buffer in the field for later DNA extraction and analysis. (79)

**Swingle, Danielle\*, and Nicole Chinnici** East Stroudsburg University, East Stroudsburg, PA 18301. *The characterization of the microbiome of american dog and deer tick mouthparts.* — American dog & deer ticks are medically important vectors, which carry pathogenic bacteria that cause diseases such as Lyme, Tularemia and Rocky Mountain spotted fever. Gaining information about the microbiome of these ticks allows for ideas about the transmission of these pathogens to be further expanded upon. Although extensive research has been conducted on the microbiome of whole ticks and tick guts, there is little information to be found about the microbiome of the mouthparts alone. Additionally, many studies focus only on pathogenic bacteria. Information about

the nonpathogenic bacteria that exist on tick mouthparts is pertinent, as both are involved in the process of tick-borne pathogen transmission to a host. This study used DNA extraction, PCR amplification, and first generation sequencing technology to characterize the nonpathogenic microbiome of American dog & deer tick capitulums, which were collected in East Stroudsburg, PA. Some of the bacterial genera identified include *Paenibacillus*, *Psuedomonas*, and *Curtobacterium*. This specific data collected can be added to the current data on the characterization of the tick microbiome, which aids in research concerning environmental control of ticks, prediction of emerging tick-borne pathogens, and the specific interactions between ticks and the bacteria they harbor. (**121**)

Teel, Jody\*, and Larry Corpus Misericordia University, Dallas, PA 18612. A Survey of Container-Breeding Mosquitoes (Insecta: Culicidae) from Selected Northeastern Pennsylvania Sites. - It is known that mosquitoes are disease vectors of malaria, Zika Virus, and other arboviruses and pose a threat to humans. The purpose of this research was to conduct a survey of container-breeding mosquito populations from selected sites in northeastern Pennsylvania to determine their distribution and abundance. Container habitats like discarded vehicle tires, litter, phytotelmata, outdoor plant vases, etc. allow for a higher distribution of mosquitoes, instead of being localized to just one large body of water. From this data, officials could evaluate whether such areas need to be sprayed for mosquitoes. Spraying can be very expensive, so it is crucial to survey before spraying. This research specifically surveyed for immature stages of mosquitoes. Water samples were collected using a turkey baster or mosquito dipper. Samples were brought back to the lab for sorting, identification, and counting. A total of 3,657 immature mosquitoes (larvae and pupae) were collected. Three different genera, Aedes, Culex, and Ochlerotatus have been identified in the samples. The majority of larval and pupal mosquitoes were in cemetery flower vases (2,058), tires (690), puddles (145), and kayaks (122). These data suggest that periodic monitoring of sites, such as cemeteries and discarded vehicle tires, would be beneficial to more accurately determine the existence, distribution, and expected numbers of adult mosquitoes prior to a serious outbreak. (138)

Thiemsen, Matthew\*, and Meg Laakso Eastern University, St. Davids, PA 19087. Coat protein samples from tomato yellow leaf curl virus and cotton leaf curl Gezira virus can be used to produce virus-specific antibodies for immune-labeling experiments. - Pathogenic plant viruses are some of the greatest threats to the agricultural industry, and outbreaks continue to occur every year. Some of these outbreaks that affect cotton plants in Africa, Pakistan, and northwestern India have been linked to cotton leaf curl virus (CLCuV). This insect-transmitted virus belongs to the Geminiviridae family and has many strains; however, the strain of interest in this study is cotton leaf curl Gezira virus (CLCuGV) which devastates crop yield in the regions where it is found, and can be associated with rapid decrease in plant resistance. To gain a better understanding of how the virus establishes an infection in host plants, visualizing the movement and cellular interactions of virus particles in host cells is necessary. In order to do this, high quality antibodies specific to the viral coat proteins is needed. Optimized coat protein gene sequences were genetically engineered for both CLCuGV and tomato yellow leaf curl virus, a well characterized relative of CLCuGV, using molecular biology techniques, and bacterial expression vectors were used to synthesize large quantities of coat protein. Using multiple reducing wash steps to separate coat protein from insoluble aggregates containing cellular protein, pure coat protein samples from each virus were isolated and sent for antibody production. The antibodies can be used for virus detection in infected tissues through dot blots, Western blots, ELISA, and immunofluorescent microscopy. Tests are being performed using infectious clones of CLCuGV and tomato vellow leaf curl virus containing the full viral DNA sequence to infect plants through agroinoculation. (34)

**Thileepan, Mathura\*, Trevor Tranchina, Robert Levenson, and Jessica Petko** Penn State University, York, PA 17403. *Characterization of interacting proteins for an alternative splice variant of the Wnt secretion molecule, Wntless.* — Wnt proteins regulate fate determination, motility,

proliferation and other developmental functions using the signal transduction pathway. Whiless (WIs) is an integral membrane protein that regulates the sorting of Wht signals. A rare splice variant of WIs, that is mainly found in primates (WIsX) has an alternate amino acid sequence in its cytoplasmic c-tail as compared to the more common splice variant. Our goal in this study was to discover proteins that specifically interact with WIsX. To identify interactors, we used a technique known as yeast two-hybrid screening. In the first type of Y2H screen used, the protein being used as bait autoactivated transcriptional activation. Therefore, a modified Membrane Yeast Two Hybrid (MYTH) was used as an alternative method. MYTH screening led to the discovery of three new interacting proteins of WIs, however these interactions were not specific to WIsX as they also interacted with the more common splice variant. One of the three novel interacting proteins, GPM6A plays an important role in neuron stem cells differentiation and migration. Future studies will focus on the interaction between WIs and GPM6A in neuronal development. (93)

Townsend, Olivia\*, Sheryl Fuller-Espie, and Sydney Stern Cabrini University, Radnor, PA 19087. Detection of antimicrobial activity of protein extracts from Eisenia hortensis using disk *diffusion methods.* — Throughout history earthworms have been used to treat various illnesses. specifically in Chinese medicine. The use of earthworms for detoxification, as an antipyretic and anesthetic, for the treatment of hypertension, inflammation, arthritis, itching, burns, carbuncles and erysipelas, and also for hastening parturition is recorded in ancient Chinese medicine books. In more recent times hemolytic, agglutinating, proteolytic, cytolytic, antipyretic, tumorstatic, anticancer, and antibacterial activities have been achieved through the use of earthworm proteins and coelomic fluid. Several earthworm extracts have shown evidence of having antibacterial activity. Glycolipoproteins and peptides acquired from different earthworm species have exhibited the ability to inhibit the growth of a number of organisms including facultative-pathogenic bacteria. Earthworm extracts could play an essential role in the future treatment of bacterial infections as many strains of bacteria are developing antibiotic resistance to one or more antibiotics. This study investigated the antibacterial activity of earthworm extracts from *Eisenia hortensis*. The extracts consisted of proteins purified from the intact earthworm using ammonium sulfate precipitation procedures. The protein extracts were tested at different doses and growth inhibition was measured using the disk diffusion method, similar to the Kirby-Bauer method used to test for efficacy of antibiotics. The protein extracts exhibited dose dependent inhibitory effects only on Pseudomonas aeruginosa and Micrococcus luteus at 250, 500 and 1000µg of total protein extract per disk. Twelve of the other bacterial strains included in the test panel did not exhibit growth inhibition. Future studies should be conducted in order to more specifically purify the proteins that exhibit antibacterial effects, for example using size exclusion, ion exchange, or hydrophobic interaction chromatography methods in order to concentrate the relevant proteins. (118)

**Tranchina, Trevor\*, Mathura Thileepan, and Jessica Petko** Penn State York, York, PA 17403. *Yeast 2-hybrid screening for novel interactors of Shrm3, a protein involved in neural tube morphogenesis.* — Shroom (Shrm) isa highly conserved family of proteins that are defined by the conservation of actin and Rho kinase binding domains.Shrm3was originally identified in a mouse mutant that displayed multiple neural tube defects.It was determined that this large proteinis involved in the organization of actinto generatemorphological changes that are required for tissue folding. In addition to the neural tube, Shroom family proteins havebeen implicated in the development of the vertebrate ear, kidney, and in brain connectivity. Little is known about what activatesShrm3function or localization. To better understand these processes we aimed to find novel protein interactors of Shrm3. Shrm3contains aPDZ domain(not critical for its function),two ASD (Apx/Shrm Domain: hallmarks of Shroom proteins), and a proline rich region (PRR). The ASD1 domain is known to directly interact with actin, and the ASD2 domain recruits the actin modifier Rhokinase(ROCK). This study utilized a classical yeast 2-hybrid screening assay to identify novel interactors of theASD-2 domain and thePRR.The screensreturned a number of novel interactors, the most interesting

beingKif3A, a motor protein sub-unit. Kif3A plays an important role in cilia formation, centriole organization, and sonic hedgehog signaling (a pathway involved in neural tube formation). Future studies are being designed to test the function of this interaction in cells and animal models. (**103**)

**Troutman, Kayla\*, and Anastasia Thévenin** Moravian College, Bethlehem, PA 18018. *Is phosphorylation a requirement for Src recruitment to the Cx43 C-terminus?* — Connexin 43 (Cx43) is a transmembrane, gap junction (GJ) protein that interacts with Src – a well-known oncogene. Since GJ channels are regulated by phosphorylations of the Cx43 C-terminus, we wanted to determine if phosphorylation plays a role in Src recruitment and inhibition. Two serine phosphorylation sites of the Cx43 C-terminus (S279 and S282) fall within the Src binding site. Through experiments both in vitro and in cells, we aim to determine if phosphorylation of S279/S282 of the Cx43 C-terminus affects its affinity for Src. Our results of in vitro binding experiments between Src and Cx43 279/282 mutants demonstrate that Src binding to Cx43 is indeed regulated through phosphorylation. Understanding molecular requirements of this interaction will allow us to design Src inhibitors using Cx43 as a recruitment scaffold. (**115**)

**Vlavianos, Stephen \*, and Daniel Ressler** Susquehanna University, Selinsgrove, PA 17870. *Analyzing stream sediments for organic matter content and carbon:nitrogen ratios as an indicator of stream health in central Pennsylvania watersheds.* — Vegetation along stream banks plays an integral role in sustaining the health of the stream, soil, aquatic life, and human quality of life. Carbon:nitrogen (C:N) ratio and loss on ignition values were obtained from stream bottom sediments and their extracts to compare local streams and determine their vulnerability to agricultural sediments from pastures and croplands. Distilled water extracts from stream sediments were analyzed using a total organic carbon and total nitrogen analyzer. Sediment sobtained a C:N of 8.4 while streams flowing between agricultural land have a lower C:N of 2.5. The quantity of organic matter from loss on ignition was not clearly correlated to stream side vegetation. These results show that stream sediment carbon:nitrogen ratios may be a reliable indicator of stream health as a simple way to monitor the effects of stream restoration projects, and could be a benchmark of a project's success. **(150)** 

Wagner, Morgan, and Christine Proctor Harrisburg University of Science and Technology, Harrisburg, PA 17101. Black bear (Ursus americanus) home range and habitat selection in Alligator National Wildlife Refuge. - The black bear (Ursus americanus) population at Alligator River National Wildlife Refuge (ARNWR) in Dare and Hyde Counties, North Carolina is believed to be one of the densest populations in the Eastern United States with an estimated density of approximately 1 bear per square kilometer (Tredick 2005). To study the relationship between habitat selection and population density within the ARNWR, forty-four black bears were fitted with GPS collars. Prior to deployment, GPS collars were remotely programmed to record locations every 5 hours with a nested program to collect a position every 30-minutes for a 5-hour period daily. The nested 30minute program was scheduled to rotate around the 24-hour clock to capture detailed movements. Due to the complex movement behavior of animals, home range analysis was determined using Brownian Bridge Movement Models. The resulting 95% home ranges were used to determine habitat selection. This study found that black bear density was positively correlated to the percentage of agricultural row crops present within a home range. It was also found that male black bears contained a higher percentage of row crops within their home ranges as compared to females. The information from this study can be used to help guide black bear habitat management decisions and hunting regulations. (43)

**Waizenegger, Zoe\*, Nicolas Thomas\*, and Julie Belanger** Kings College, Wilkes-Barre, PA 18711. *Characterization of thermal transitions of dipalmitoylphosphatidylcholine lipids in the presence of small molecules with differential scanning calorimetry.* — Small hydrophobic molecules can be used as payloads within drug delivery vehicles, such as liposomes. Characterization of the

thermotropic behavior is needed to better understand the stability and release of drugs. Differential scanning calorimetry (DSC) is a technique that has been used to analyze the thermotropic phase behavior of many biological compounds, such as lipids. Phosphatidylcholine lipids, when dispersed in an aqueous milieu, form bilayer membrane structures that undergo phase transitions when being analyzed by DSC. Previous research with the addition of small hydrophobic molecules, such as Nphenyl-1-naphthylamine (NPN), to hydrated lipid membranes shows a shift in this melting transition. To our knowledge, the effect of the introduction of both cholesterol and NPN in varying amounts has not been explored. This research used DSC to characterize the main transition in dipalmitoylphosphatidylcholine (DPPC) liposomes in the presence of NPN and cholesterol. The trends observed through this project have been lower onset melting temperatures, lower enthalpies of reaction, and lower peak melting temperatures in the presence of cholesterol and NPN when compared to controls when compared to controls. The accepted value for the melting transition of DPPC liposomes is 41.0°C. The results of this ongoing research show that there is a decrease by 1.0°C to the melting transition of liposomes when NPN or cholesterol are added. However, when both NPN and cholesterol are incorporated together the melting transition of liposomes decrease by 1.5°C. When comparing the various treatments with DPPC liposome negative control, the melting transitions were statistically different from each other, whereas the data sets for the enthalpy values were statistically the same as each other. These findings provide a step towards further quantifying the additive effects of the thermotropic behavior of small hydrophobic drugs within the membrane bilayer. (162)

Walter, Cynthia\*, Elaine Bennett, Haley Farrie, Haley Adams, Melissa Anderson, Brandon Snyder, and Lindsay Richardson Saint Vincent College, Latrobe, PA 15650. Students document fecal contamination in underserved rural areas: Results from Solola', Guatemala and Pennsylvania, USA. - Students document fecal contamination in underserved rural areas: Results from Solola', Guatemala and Pennsylvania, USA - Fecal contamination of water or foods is a major public health concern, but costs of professional testing severely restrict monitoring. These issues are significant in rural areas in underdeveloped nations with irregular management of community water supplies. domestic animal waste and house fly abundance. Limited testing for contamination is also important in US states such as Pennsylvania that do not require or fund private well testing. In these underserved areas, undergraduate students can reliably perform simple tests and provide preliminary data to help experts and citizens take corrective actions. In Guatemala, multi-year collaborations of indigenous community organizations in Mayan villages around Lake Atitlan engage citizens with undergraduate students from the USA to study health issues. They report fecal bacteria presence in 20-50% of household taps fed by different, small, municipal sources. House flies are abundant and 100% of flies collected from kitchens held fecal bacteria. Over 60% of dog feces indicated infection with Giardia, Cryptosporidium or both parasites in street dogs. In response to this information, citizens and experts are increasing efforts to reduce risks of infection from fecal pathogens. In rural Southwestern Pennsylvania, over 30% of private water wells tested from 2014-2017 contained fecal Escherichia coli and/or hydrogen sulfide producing bacteria. Most homeowners have not had their water tested for several years, many have no water treatment or filter only for chemicals, for example, to remove substances from prior or current industrial contamination. These results are similar to those in a larger study across Pennsylvania, a state where 3 million residents rely on private well water. Projects in these two countries indicate rural areas share problems with fecal contamination, trained undergraduates can play a role to identify pollution sources and citizens are eager to gain information and take steps to address this important component of public health. (155)

**Wasser, Adam\*, Peter Stapleford\*, and Robert Major** Indiana University of Pennsylvania, Indiana, PA 15705. *PCR-Based Cloning of Genes from the Freshwater Planarian, <u>Schmidtea</u> <u>Mediterranea</u>. — The freshwater planarian has become a preferred model system for understanding the cellular and molecular mechanisms governing complex tissue regeneration. Along with an*  amazing capacity to repair every cell type following amputation, the planarian is amenable to techniques that report on gene expression pattern and function. In order to functionally examine a gene's role in tissue regeneration, we will use RNA interference (RNAi) to inhibit gene activity in injured animals. To this end, we have used the Polymerase Chain Reaction to amplify seven genes from a cDNA library. We have ligated these DNA fragments into cloning vectors and have verified the cloned products through DNA sequencing. We are constructing double-stranded RNA to use in subsequent RNAi experiments. Our findings will unveil new details regarding the tissue repair process due to aging and tissue damage. (72)

Williams, Ashley\*, and Angela Asirvatham Misericordia University, Dallas, PA 18612. Dose response effects of forskolin on immortalized Schwann cell growth. - Schwann cell growth in vitro is stimulated by heregulin, a neuronal growth factor and mitogens that activate cyclic AMP, the universal cellular second messenger. Schwann cell proliferation versus myelination is orchestrated by a balance between mitogens and promyelinating factors. While the pattern of Schwann cell growth in response to mitogens has been well characterized in primary cultures, the concentration of forskolin, a pharmacological activator of cAMP that stimulate proliferation in cell lines are unknown. This study was undertaken to determine the concentration of forskolin that promotes optimal cell growth, secretion of cAMP, and expression of downstream signaling effectors such as A-Kinase Anchoring Proteins (AKAPs). It was hypothesized that an increase in forskolin dosage will elicit a dose-dependent rise in cell proliferation, cAMP levels and expression of AKAPs. Immortalized Schwann cells were cultured with no mitogens, 12.5 ng/ml heregulin, various doses of forskolin at 0.5 µM, 1 µM, 2 µM or 3 µM and heregulin + forskolin for 4, 6, 12 or 24 hours and analyzed for growth using the MTT proliferation assay. A time-dependent cell growth was observed in cultures incubated with 0.5 µM forskolin or heregulin + forskolin, while higher concentrations decreased proliferation and cAMP levels after 12 hours. In contrast, cells treated for 24 hours with heregulin and 1 µM or 2 µM forskolin displayed a dose-dependent increase in growth and cAMP levels. At concentrations of 3 µM, 24 hour cultures exhibited an increase in cAMP levels even when cell growth was diminished. Immunoblot analysis of AKAPs from 12 and 24 hour cultures exhibited a differential expression with various doses of the mitogens. These preliminary findings indicate that increasing concentration of forskolin and incubation time promotes Schwann cell growth, while dosage above 2 µM limits proliferation, cAMP secretion and expression of AKAPs. (55)

Yingst, Amber\*, Mara Menk, Josh Shaffer, Elizabeth Smith, and Dr. Daniel Widzowski Indiana University of Pennsylvania, Indiana, PA 15705. Effects of the antihistamine fexofenadine on body weight, body fat, blood glucose, and serum and liver triglycerides in mice. - Diets high in saturated fats and antihistamine-administration have both been implicated in metabolic disorders in animal models and in humans. The interaction of these factors is poorly understood. Omega-3 hepatoprotection has not been well studied in relation to drug-diet interactions. The present study examined the role of a high fat diet (45% lard) or low fat (10% lard) or an omega-3 fatty acid (O3FA) enriched diet (45% menhaden oil) and sub-chronic administration of the antihistamine fexofenadine on metabolic disturbances in C57BI/6J mice. Two subchronic (14 day or less) experiments found significant increases in body weight when fexofenadine was administered with a high (45%) lard diet but not with either low fat (10% lard) or a 45% O3FA diet. Furthermore, these effects occurred in the first two weeks of drug administration, suggesting rapid effects of drugs and diet on metabolism and body weight regulation. Fexofenadine administration resulted in increased perigonadal fat pad weights and liver weights. Mice fed the omega-3 diet showed unchanged body weights. These results suggest that fexofenadine administration can induce changes in body weight that are dependent on dietary fat content. Ongoing and future experiments will examine the levels of serum and liver triglycerides to provide a fuller picture of the metabolic effects of dietary fat (45% lard, 10% lard or O3FA) and fexofenadine treatments. (95)

**Zaneski, Rebecca\*, and Cosima Wiese** Misericordia University, Dallas, PA 18612. Comparison of Multiple Techniques in Quantifying Impacts of Elevated zinc Concentrations on Growth and

Reproduction of Lemna minor. - Lemna minor (duckweed), from the family Lemnaceae, is a small flowering plant found in wet environments worldwide (Hurd and Sternberg, 2008). As a primary producer, L. minor is a useful system for studies investigating impacts of pollutants on aquatic ecosystems because it can absorb pollutants through its roots as it rests on the surface of the water (Horvat et al., 2007; Hurd and Sternberg, 2008; Khellaf and Zerdaoui, 2009; Lewis, 1995; Naumann et al., 2006). The goal of this research was to determine the impacts of elevated concentrations of zinc on the growth and asexual reproduction of *L. minor*, and to compare multiple techniques for guantifying effects on growth. It was hypothesized that leaf area will more accurately characterize impacts of zinc on L. minor than biomass, due to the small size of the organism and the difficulty in obtaining accurate biomass measurements. To test this, L. minor fronds were grown in a modified Hoagland's solution with elevated concentrations of zinc ranging from 0 to 17.5 mg/l zinc in a growth chamber. After a 7 day exposure, biomass, leaf area and chlorophyll content were measured. Initial results with untreated L. minor samples showed a highly significant correlation between biomass and leaf area measurements, indicating that leaf area can be used as a proxy measure for biomass. Increasing concentrations of zinc caused reductions in biomass and chlorophyll a and b content in the duckweed samples. Declining chlorophyll content suggests decreases in the photosynthetic rate, leading to impacts on growth and reproduction. Changes in leaf area were difficult to ascertain due to limitations of the software selected for leaf area measurements. (48)